

SOURCE
ORGANISM
Engraulis encrasicolus (European anchovy)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Clupeiformes;
Engraulidae; Engraulis.
REFERENCE
1 (bases 1 to 216)

AUTHORS
Moran, P.
TITLE
Direct Submission
JOURNAL
Submitted (17-DEC-2001) Genetica, Universidad de Vigo, Campus
Lagoas Marcosende, Vigo 36200, Spain
FEATURES
source
Location/Qualifiers
1..216

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/organelle="mitochondrion"
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ORIGIN

Query Match 100.0%; Score 25; DB 5; Length 216;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25

Db 188 TACCATGAGGACAAATATCATCTG 212

RESULT 3
AF145511
LOCUS
DEFINITION
Melanoplus angustipennis cytochrome b gene, partial cds;
mitochondrial gene for mitochondrial product.
ACCESSION
AF145511
VERSION
AF145511.1 GI:5918571

KEYWORDS
SOURCE
mitochondrion Melanoplus angustipennis (narrowwinged sand
grasshopper)

ORGANISM
Melanoplus angustipennis
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Melanoplinae; Melanoplus.
1 (bases 1 to 258)

REFERENCE
AUTHORS
Chapco, W., Kuperus, W.R. and Litzzenberger, G.S.
TITLE
Molecular phylogeny of melanoplinae grasshoppers (Orthoptera:
Acrididae). The genus Melanoplus

JOURNAL
Ann. Entomol. Soc. Am. 92 (5), 617-623 (1999)

REFERENCE
AUTHORS
Chapco, W., Kuperus, W.R. and Litzzenberger, G.S.

TITLE
Direct Submission
JOURNAL
Submitted (23-APR-1999) Biology, University of Regina, 3737 Wascana
Parkway, Regina, Saskatchewan S4S 0A2, Canada
FEATURES
source
Location/Qualifiers
1..258

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CDS

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25

Db 169 TACCATGAGGACAAATATCATCTG 193

RESULT 4

AF145531

LOCUS

DEFINITION
Melanoplus foedus cytochrome b gene, partial cds; mitochondrial

ACCESSION
AF145531

VERSION
AF145531.1 GI:5918591

KEYWORDS

SOURCE

ORGANISM

Melanoplus foedus

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;

Acridoidea; Acrididae; Melanoplinae; Melanoplus.
1 (bases 1 to 258)

REFERENCE
AUTHORS
Chapco, W., Kuperus, W.R. and Litzzenberger, G.S.

TITLE
Molecular phylogeny of melanoplinae grasshoppers (Orthoptera:
Acrididae). The genus Melanoplus

JOURNAL
Ann. Entomol. Soc. Am. 92 (5), 617-623 (1999)

REFERENCE
AUTHORS
Chapco, W., Kuperus, W.R. and Litzzenberger, G.S.

TITLE
Direct Submission

JOURNAL
Submitted (23-APR-1999) Biology, University of Regina, 3737 Wascana
Parkway, Regina, Saskatchewan S4S 0A2, Canada
FEATURES
source
Location/Qualifiers
1..258

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/db_xref="GI:5918650"
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CDS

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Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25

Db 169 TACCATGAGGACAAATATCATCTG 193

RESULT 5

AF317194

LOCUS

DEFINITION
Barytettix humphreysi cytochrome b gene, partial cds; mitochondrial

ACCESSION
AF317194

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VERSION      AF317194.1  GI:33337314
KEYWORDS
SOURCE       mitochondrial Barytettix humphreysi
ORGANISM     Barytettix humphreysi
             Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
             Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
             Acridoidea; Acrididae; Melanoplinae; Barytettix.
REFERENCE    1 (bases 1 to 258)
AUTHORS      Litzenberger, G.S. and Chapco, W.
TITLE        Direct Submission
JOURNAL      Submitted (26-OCT-2000) Department of Biology, University of
             Regina, 3737 Wascana Parkway, Regina, Saskatchewan S4S 0A2, Canada
FEATURES     source
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             /organism="Barytettix humphreysi"
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Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
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Db 169 TACCATGAGGACAAATATCATCTG 193

RESULT 6
LOCUS      AY004180
DEFINITION Parapodisma mikado cytochrome b gene, partial cds; mitochondrial
             gene for mitochondrial product.
ACCESSION  AY004180
VERSION     AY004180.1  GI:20451280
KEYWORDS
SOURCE      mitochondrial Parapodisma mikado
ORGANISM     Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
             Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
             Acridoidea; Acrididae; Catantopinae; Parapodisma.
REFERENCE    1 (bases 1 to 258)
AUTHORS      Litzenberger, G. and Chapco, W.
TITLE        Molecular Phylogeny of Selected Eurasian Podismine Grasshoppers
             (Orthoptera: Acrididae)
JOURNAL      Ann. Entomol. Soc. Am. 94 (4), 505-511 (2001)
REFERENCE    2 (bases 1 to 258)
AUTHORS      Litzenberger, G.S. and Chapco, W.
TITLE        Direct Submission
JOURNAL      Submitted (04-JUL-2000) Biology, University of Regina, 3737 Wascana
             Parkway, Regina, Saskatchewan S4S 0A2, Canada
FEATURES     source
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LVMATAFMGVLPWGQMSFWGATVITNLLSAIPYLGLDLVQ"
ORIGIN
Query Match      100.0%; Score 25; DB 3; Length 258;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
    |||||||||||||||||||
Db 169 TACCATGAGGACAAATATCATCTG 193

RESULT 7
LOCUS      AY004205
DEFINITION Primnoa litoralis cytochrome b gene, partial cds; mitochondrial
             gene for mitochondrial product.
ACCESSION  AY004205
VERSION     AY004205.1  GI:20451330
KEYWORDS
SOURCE      mitochondrial Primnoa litoralis
ORGANISM     Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
             Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
             Acridoidea; Acrididae; Catantopinae; Primnoa.
REFERENCE    1 (bases 1 to 258)
AUTHORS      Litzenberger, G. and Chapco, W.
TITLE        Molecular Phylogeny of Selected Eurasian Podismine Grasshoppers
             (Orthoptera: Acrididae)
JOURNAL      Ann. Entomol. Soc. Am. 94 (4), 505-511 (2001)
REFERENCE    2 (bases 1 to 258)
AUTHORS      Litzenberger, G.S. and Chapco, W.
TITLE        Direct Submission
JOURNAL      Submitted (04-JUL-2000) Biology, University of Regina, 3737 Wascana
             Parkway, Regina, Saskatchewan S4S 0A2, Canada
FEATURES     source
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ORIGIN
Query Match      100.0%; Score 25; DB 3; Length 258;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
    |||||||||||||||||||
Db 169 TACCATGAGGACAAATATCATCTG 193

RESULT 8
LOCUS      CCU17904
DEFINITION Circotettix carlinianus mitochondrial cytochrome b gene, partial
             cds.

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ACCESSION      U17904
VERSION        U17904.1  GI:601796
KEYWORDS
SOURCE         mitochondrion Aerochoreutes carlinianus
ORGANISM       Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
               Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
               Acridoidea; Acrididae; Oedipodinae; Aerochoreutes.
REFERENCE      1 (bases 1 to 258)
AUTHORS       Chapco,W. and Martel,R.K.B.
TITLE         Mitochondrial DNA sequence variation in North American hand-winged
               grasshoppers
JOURNAL        Unpublished
REFERENCE      2 (bases 1 to 258)
AUTHORS       Chapco,W.
TITLE         Direct Submission
JOURNAL        Submitted (01-DEC-1994) Chapco W., University of Regina, Biology,
               Regina, Saskatchewan, Canada, S4S 0A2
               Location/Qualifiers
FEATURES       1..258
               /organism="Aerochoreutes carlinianus"
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               /db_xref="taxon:36992"
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               LVMATAFMGYVLPWGQMSFWGATVITNLSAIPYIGTDIVQ"

CDS
LOCUS          SCU18257          258 bp    DNA    linear    INV 27-JAN-1995
DEFINITION     Spargemom collare cytochrome b gene, mitochondrial gene encoding
               mitochondrial protein, partial cds.
ACCESSION      U18257
VERSION        U18257.1  GI:624181
KEYWORDS
SOURCE         mitochondrion Spargemom collare (mottled sand grasshopper)
ORGANISM       Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
               Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
               Acridoidea; Acrididae; Oedipodinae; Spargemom.
REFERENCE      1 (bases 1 to 258)
AUTHORS       Chapco,W. and Martel,R.K.B.
TITLE         Mitochondrial DNA sequence variation in North American band-winged
               grasshoppers
JOURNAL        Unpublished
REFERENCE      2 (bases 1 to 258)
AUTHORS       Chapco,W.
TITLE         Direct Submission
JOURNAL        Submitted (06-DEC-1994) William Chapco, University of Regina,
               Biology, Regina, Saskatchewan, S4S 0A2, Canada
               Location/Qualifiers
FEATURES       1..258
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ORIGIN
Query Match      100.0%; Score 25; DB 3; Length 258;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TACCATGAGGACAAATATCATCTG 25
        |||||||
DB      169 TACCATGAGGACAAATATCATCTG 193

RESULT 10
LOCUS      SCU18257          258 bp    DNA    linear    INV 27-JAN-1995
DEFINITION     Spargemom collare cytochrome b gene, mitochondrial gene encoding
               mitochondrial protein, partial cds.
ACCESSION      U18257
VERSION        U18257.1  GI:624181
KEYWORDS
SOURCE         mitochondrion Spargemom collare (mottled sand grasshopper)
ORGANISM       Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
               Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
               Acridoidea; Acrididae; Oedipodinae; Spargemom.
REFERENCE      1 (bases 1 to 258)
AUTHORS       Chapco,W. and Martel,R.K.B.
TITLE         Mitochondrial DNA sequence variation in North American band-winged
               grasshoppers
JOURNAL        Unpublished
REFERENCE      2 (bases 1 to 258)
AUTHORS       Chapco,W.
TITLE         Direct Submission
JOURNAL        Submitted (06-DEC-1994) William Chapco, University of Regina,
               Biology, Regina, Saskatchewan, S4S 0A2, Canada
               Location/Qualifiers
FEATURES       1..258
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Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TACCATGAGGACAAATATCATCTG 25
        |||||||
DB      169 TACCATGAGGACAAATATCATCTG 193

RESULT 9
CPUI8250
LOCUS      CPU18250          258 bp    DNA    linear    INV 27-JAN-1995
DEFINITION     Cammulla pellucida cytochrome b gene, mitochondrial gene encoding
               mitochondrial protein, partial cds.
ACCESSION      U18250
VERSION        U18250.1  GI:624167
KEYWORDS
SOURCE         mitochondrion Cammulla pellucida (clear-winged grasshopper)
ORGANISM       Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
               Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
               Acridoidea; Acrididae; Oedipodinae; Cammulla.
REFERENCE      1 (bases 1 to 258)
AUTHORS       Chapco,W. and Martel,R.K.B.
TITLE         Mitochondrial DNA sequence variation in North American band-winged
               grasshoppers
JOURNAL        Unpublished
REFERENCE      2 (bases 1 to 258)
AUTHORS       Chapco,W.
TITLE         Direct Submission
JOURNAL        Submitted (06-DEC-1994) William Chapco, University of Regina,
               Biology, Regina, Saskatchewan, S4S 0A2, Canada
               Location/Qualifiers
FEATURES       1..258
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               /organelle="mitochondrion"

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RESULT 11
SCU18258
LOCUS
DEFINITION
Spharagemon campestris cytochrome b gene, mitochondrial gene
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
mitochondrion Spharagemon campestris
Spharagemon campestris
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Oedipodinae; Spharagemon.
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
2 (bases 1 to 258)
Chapco,W.
Direct Submission
Submitted (06-DEC-1994) William Chapco, University of Regina,
Biology, Regina, Saskatchewan, S4S 0A2, Canada
FEATURES
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1..258
/organism="Spharagemon campestris"
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/db_xref="GI:624184"
/translation="IIRTHANGAMLFFICIVLHVGRGIYGSYMYMTWTGTWMLF
LVMTAFMGYVLPWGQMSFWGATVITNLLSAIPYMGTEIVQ"

CDS
1 TACCATGAGGACAAATATCATCTG 25
169 TACCATGAGGACAAATATCATCTG 193

ORIGIN
Query Match 100.0%; Score 25; DB 3; Length 258;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 TACCATGAGGACAAATATCATCTG 25
169 TACCATGAGGACAAATATCATCTG 193

Db

RESULT 12
TPU18253
LOCUS
DEFINITION
Trimerotropis pistrinaria cytochrome b gene, mitochondrial gene
encoding mitochondrial protein, partial cds.
ACCESSION
VERSION
KEYWORDS
SOURCE
mitochondrion Trimerotropis pistrinaria
Trimerotropis pistrinaria
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
Acridoidea; Acrididae; Oedipodinae; Trimerotropis.
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
2 (bases 1 to 258)
Chapco,W. and Martel,R.K.B.
Mitochondrial DNA sequence variation in North American band-winged
grasshoppers
Unpublished
Chapco,W.
Direct Submission
Submitted (06-DEC-1994) William Chapco, University of Regina,
Biology, Regina, Saskatchewan, S4S 0A2, Canada
FEATURES
source
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/organism="Spharagemon campestris"
/organelle="mitochondrion"
/mol_type="genomic DNA"
/isolate="Last Mountain Lake, Saskatchewan"
/db_xref="taxon:37256"
/tissue_type="whole organism minus gut"
/dev_stage="adult"
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/codon_start=3
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/product="cytochrome b"
/protein_id="AAA61679.1"
/db_xref="GI:624184"
/translation="IIRTHANGAMLFFICIVLHVGRGIYGSYMYMTWTGTWMLF
LVMTAFMGYVLPWGQMSFWGATVITNLLSAIPYMGTEIVQ"

CDS
1 TACCATGAGGACAAATATCATCTG 25
169 TACCATGAGGACAAATATCATCTG 193

ORIGIN
Query Match 100.0%; Score 25; DB 3; Length 258;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 TACCATGAGGACAAATATCATCTG 25
169 TACCATGAGGACAAATATCATCTG 193

Db

RESULT 13
AF371961
LOCUS
DEFINITION
Bos taurus cytochrome b (cytb) gene, partial cds; mitochondrial
gene for mitochondrial product.
ACCESSION
VERSION
KEYWORDS
SOURCE
mitochondrion Bos taurus (cow)
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
2 (bases 1 to 279)
Bottero,M.T., Civera,T., Anastasio,A., Turi,R.M. and Rosati,S.
Identification of cow's milk in 'buffalo' cheese by duplex
polymerase chain reaction
J. Food Prot. 65 (2), 362-366 (2002)
21837100
11848568
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
1..279
/organism="Bos taurus"
/organelle="mitochondrion"
/mol_type="genomic DNA"
/db_xref="taxon:9913"
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/product="cytochrome b"
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/db_xref="GI:14091673"
/translation="GLYGSYTFEFTNIGVILLTVMATAFMGYVLPWGQMSFWGAT
VITNLLSAIPYIGTNLVEWGWGSKATLTFFAHFILPFIIMAA"

TITLE
JOURNAL
Submitted (06-DEC-1994) William Chapco, University of Regina,
Biology, Regina, Saskatchewan, S4S 0A2, Canada
FEATURES
source
1..258
/organism="Trimerotropis pistrinaria"
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CDS
1 TACCATGAGGACAAATATCATCTG 25
169 TACCATGAGGACAAATATCATCTG 193

ORIGIN
Query Match 100.0%; Score 25; DB 3; Length 258;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 TACCATGAGGACAAATATCATCTG 25
169 TACCATGAGGACAAATATCATCTG 193

Db

RESULT 14
AF371961
LOCUS
DEFINITION
Bos taurus cytochrome b (cytb) gene, partial cds; mitochondrial
gene for mitochondrial product.
ACCESSION
VERSION
KEYWORDS
SOURCE
mitochondrion Bos taurus (cow)
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
2 (bases 1 to 279)
Bottero,M.T. and Rosati,S.
Direct Submission
Submitted (18-APR-2001) Produzioni Animali, Facolta' di Medicina
Veterinaria, Via Nizza, 52, Torino, TO 10126, Italy
FEATURES
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1..279
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/transl_table=2
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ORIGIN

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 Matches 25; Conservative 0; Mismatches 0;

Qy 1 TACCATGAGGACAAATATCATCTG 25
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Db 98 TACCATGAGGACAAATATCATCTG 122
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RESULT 14

S49215 279 bp DNA linear MAM 05-AUG-1999
 LOCUS apocytochrome b [sheep, domestic, Merinolandschaf, liver,
 DEFINITION Mitochondrial, 279 nt].

ACCESSION S49215 GI:259294

KEYWORDS

SOURCE

ORGANISM

mitochondrion Ovis aries (sheep)
 Ovis aries
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Caprinae; Ovis.

REFERENCE

1 (bases 1 to 279)

AUTHORS

Hiendleder, S., Hecht, W., Dzapo, V. and Wassmuth, R.

TITLE

Ovine mitochondrial DNA: restriction enzyme analysis, mapping and
 sequencing data

JOURNAL

MEDLINE

PUBMED

REMARK

93073120

1332554

GenBank staff at the National Library of Medicine created this
 entry [NCBI gisseq 117456] from the original journal article.

FEATURES

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ORIGIN

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 Matches 25; Conservative 0; Mismatches 0;

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Db 56 TACCATGAGGACAAATATCATCTG 80
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RESULT 15

AY217671

LOCUS

AY217671 290 bp mRNA linear VRT 01-JUN-2003
 DEFINITION Xenopus laevis isolate 3 from South Africa cytochrome b (cytb)
 mRNA, partial cds; mitochondrial gene for mitochondrial product.

ACCESSION

AY217671

VERSION

KEYWORDS

SOURCE

ORGANISM

mitochondrion Xenopus laevis (African clawed frog)
 Xenopus laevis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1..290

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/organelle="mitochondrion"

/mol_type="mRNA"

/isolate="3"

/db_xref="taxon:8355"

/country="South Africa: Pearly Beach"

/note="isolated by JM & AC"

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<1..>290

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/transl_table=3

/product="cytochrome b"

/protein_id="AAP21010.1"

/db_xref="GI:3122352"

/translation="TGLFLAMHYTADTSMAFSSVAHICRDVNYGWLIRNLHANGASPF
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ORIGIN

Query Match

Best Local Similarity

Matches

25; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

Qy

1

TACCATGAGGACAAATATCATCTG

25

|||||

Db

262

TACCATGAGGACAAATATCATCTG

286

|||||

Search completed:

November 17, 2004, 02:58:37

Job time : 138.759 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 22:24:28 ; Search time 357.388 Seconds
(without alignments)
2650.992 Million cell updates/sec

Title: US-09-821-782E-2

Perfect score: 26

Sequence: 1 cctcctagttttagggattgatcg 26

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	24.4	93.8	132	2	BE487586 176420 BA
C 2	24.4	93.8	147	7	CR383176 CR383176
C 3	24.4	93.8	188	6	CB226256 IRT31H03
C 4	24.4	93.8	250	6	CB227362 IRT31H03
C 5	24.4	93.8	256	6	CB221363 IRT31H03
C 6	24.4	93.8	293	6	CD288296 3.P21.abd
C 7	24.4	93.8	300	7	CK959074 4059657 B
C 8	24.4	93.8	304	4	BM434693 IRT11H08
C 9	24.4	93.8	322	4	BM434895 IRT15D07
C 10	24.4	93.8	324	4	B1538794 434369 MA
C 11	24.4	93.8	328	1	AJ693580 AJ693580
C 12	24.4	93.8	330	4	BM435757 IRT31H03
C 13	24.4	93.8	330	7	CK727400 UMC-bend
C 14	24.4	93.8	331	2	BE487585 176419 BA
C 15	24.4	93.8	331	7	CN998120 UMC-bcl_0
C 16	24.4	93.8	333	2	BF429485 1014 MARC
C 17	24.4	93.8	333	7	CK729034 UMC-bend
C 18	24.4	93.8	338	4	BM435844 IRT5A12.a
C 19	24.4	93.8	339	7	CN654035 UMC-bcl_0
C 20	24.4	93.8	342	2	BF429697 1465 MARC
C 21	24.4	93.8	342	5	BP103466 BP103466
C 22	24.4	93.8	343	4	BM434542 IRT06A12
C 23	24.4	93.8	344	7	CK728189 UMC-bend
C 24	24.4	93.8	344	7	CN653932 UMC-bcl_0

25	24.4	93.8	344	7	CO000574
26	24.4	93.8	345	7	CK730086
27	24.4	93.8	347	7	CO727212
28	24.4	93.8	348	4	BM434469
29	24.4	93.8	351	7	CN654069
30	24.4	93.8	351	7	CO000322
31	24.4	93.8	351	7	CN654050
32	24.4	93.8	353	7	CO728674
33	24.4	93.8	353	7	CN999365
34	24.4	93.8	354	7	CN999365
35	24.4	93.8	355	6	CB226824
36	24.4	93.8	355	7	CK729003
37	24.4	93.8	356	5	BP102696
38	24.4	93.8	356	7	CN654406
39	24.4	93.8	357	6	CB226333
40	24.4	93.8	358	1	AU277856
41	24.4	93.8	359	7	CK983106
42	24.4	93.8	360	4	BM434466
43	24.4	93.8	360	4	BM436089
44	24.4	93.8	360	7	CK729336
45	24.4	93.8	362	4	BM436122

ALIGNMENTS

RESULT 1
BE487586/c
LOCUS BE487586 176420 BARC 5BOV Bos taurus cDNA 5', mRNA linear EST 27-MAR-2003
DEFINITION BE487586
ACCESSION BE487586
VERSION BE487586.1 GI:9607119
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 132)
AUTHORS Sonstegard,T., Capuco,A.V., White,J., Van Tassel,C.P., Connor,E.E., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D. and Quackenbush,J.
TITLE Analysis of bovine mammary gland EST and functional annotation of the Bos taurus gene index
JOURNAL Mamm. Genome 13 (7), 373-379 (2002)
MEDLINE 22135956
PUBMED 12140684
COMMENT Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tad@psi.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCCAGTCACGACG
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Seq primer: ATTAGTGACACTATAG.

FEATURES

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ORIGIN
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Best Local Similarity 96.2%; Pred. No. 1;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTCCTAGTTTGTAGGGATTGATCG 26
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Db 61 CCTCCTAGTTTGTGGGATTGATCG 36

RESULT 2
CR383176/c
LOCUS
DEFINITION
CR383176 Bovine multi-stage muscles library (bcas) Bos taurus cDNA
clone bcas0003a.f.03 5prim, mRNA sequence.
ACCESSION
CR383176
VERSION
CR383176.1 GI:47005080
KEYWORDS
EST.
SOURCE
Bos taurus (cow)
ORGANISM
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE
1 (bases 1 to 147)
AUTHORS
Chevalet, C.
TITLE
AGENAE, a French Animal Genome project
JOURNAL
Unpublished (2004)
COMMENT
Contact: Martin P
INRA, Genomique & Physiologie de la Lactation
Domaine de Vilvert, 78352 JOUY-EN-JOSAS cedex, FRANCE
Tel: +33 (0) 1.34.65.25.82
Fax: +33 (0) 1.34.65.29.26
Email: Patrice.Martin@jouy.inra.fr
Sequence cleaned of vector, adaptor and repetitions. Contact us
at signenasupport@jouy.inra.fr to obtain the chromatogram of this
sequence.
Plate: 0003 row: f column: 3.
FEATURES
Location/Qualifiers
1..147
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/db_xref="taxon:9913"
/clone="bcas0003a.f.03"
/tissue_type="muscles : heart, longissimus thoracis,
semitendinosus, masseter, cutaneous trunci"
/dev_stages="from embryos to adults"
/clone_lib="Bovine multi-stage muscles library (bcas)"
/note="Clone distribution : AGENAE Resource centre.
Francois PIUMI, Francois.Piumi@jouy.inra.fr, INRA, CEA
Radiobiologie et Etude du genome (LREG), Domaine de
Vilvert, 78352, Jouy-en-Josas cedex, FRANCE, +33 (0)
1.34.65.28.02, +33 (0) 1.34.65.22.73"

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Best Local Similarity 96.2%; Pred. No. 1;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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CB226256/c
LOCUS
DEFINITION
CB226256 Bos taurus Reticulum #1 library Bos taurus cDNA, mRNA
sequence.
ACCESSION
CB226256
VERSION
CB226256.1 GI:28296770
KEYWORDS
EST.
SOURCE
Bos taurus (cow)

ORIGIN
Query Match          93.8%; Score 24.4; DB 6; Length 188;
Best Local Similarity 96.2%; Pred. No. 1.1;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTCCTAGTTTGTAGGGATTGATCG 26
    |||||
Db 158 CCTCCTAGTTTGTGGGATTGATCG 133

RESULT 4
CB227362/c
LOCUS
DEFINITION
CB227362 Bos taurus Rumen #1 library Bos taurus cDNA, mRNA
sequence.
ACCESSION
CB227362
VERSION
CB227362.1 GI:28297876
KEYWORDS
EST.
SOURCE
Bos taurus (cow)
ORGANISM
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE
1 (bases 1 to 250)
AUTHORS
Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Sensen, C.W.,
Gordon, P.M.K. and Moore, S.S.
TITLE
Gene Expression Profiling of the Bovine Gastrointestinal Tract
JOURNAL
Unpublished (2002)
COMMENT
Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
Tel: 780 492 0169
Fax: 780 492 4285
Email: stephen.moore@ualberta.ca
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Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DEFINITION
CB227362 Bos taurus Rumen #1 library Bos taurus cDNA, mRNA
sequence.
ACCESSION
CB227362
VERSION
CB227362.1 GI:28297876
KEYWORDS
EST.
SOURCE
Bos taurus (cow)
ORGANISM
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE
1 (bases 1 to 250)
AUTHORS
Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Sensen, C.W.,
Gordon, P.M.K. and Moore, S.S.
TITLE
Gene Expression Profiling of the Bovine Gastrointestinal Tract
JOURNAL
Unpublished (2002)
COMMENT
Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
Tel: 780 492 0169
Fax: 780 492 4285
Email: stephen.moore@ualberta.ca
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Site_2: Xho I"

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Best Local Similarity 96.2%; Pred. No. 1.1;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTTGTAGGGATTGATCG 26
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Db 74 CCTCCTAGTTTGTGGGATTGATCG 49

RESULT 5
CB221363/c
LOCUS      CB221363      256 bp      mRNA      linear      EST 10-FEB-2003
DEFINITION 1duo05F04 Bos taurus Duodenum #1 library Bos taurus cDNA, mRNA
sequence.
ACCESSION  CB221363
VERSION    CB221363.1 GI:28291877
KEYWORDS   EST.
SOURCE     Bos taurus (cow)
ORGANISM   Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE  1 (bases 1 to 256)
AUTHORS   Hansen,C., Fu,A., Meng,Y., Li,C., Okine,E., Sensen,C.W.,
Gordon,P.M.K. and Moore,S.S.
TITLE     Gene Expression Profiling of the Bovine Gastrointestinal Tract
JOURNAL   Unpublished (2002)
COMMENT   Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
Tel: 780 492 0169
Fax: 780 492 4265
Email: stephen.moore@ualberta.ca
Insert Length: 256 Std Error: 0.00
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/lab_host="XLI-BlueMRF strain"
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Site_1: EcoRI; Site_2: Xho I"

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Best Local Similarity 96.2%; Pred. No. 1.1;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTTGTAGGGATTGATCG 26
    |||||||
Db 154 CCTCCTAGTTTGTGGGATTGATCG 129

RESULT 6
CD288296
LOCUS      CD288296      293 bp      mRNA      linear      EST 27-MAY-2003
DEFINITION 3 P21.abd POE14 (Day_14_pregnant_ovine_endometrium) Ovis aries
cDNA, mRNA sequence.

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ACCESSION  CD288296
VERSION    CD288296.1 GI:31086339
KEYWORDS   Ovis aries (sheep)
SOURCE     Ovis aries
ORGANISM   Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Caprinae; Ovis.
REFERENCE  1 (bases 1 to 293)
AUTHORS   Gray,C.A., Adelson,D.L. and Spencer,T.E.
TITLE     Ovine ESTs
JOURNAL    Unpublished (2003)
COMMENT   Contact: Thomas E. Spencer
Center for Animal Biotechnology and Genomics
Texas A&M University
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
USA
Tel: 9798454896
Fax: 9798622662
Email: tspencer@ansc.tamu.edu.
Location/Qualifiers
1..293
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method and pooled from 5 females."

ORIGIN
Query Match      93.8%; Score 24.4; DB 6; Length 293;
Best Local Similarity 96.2%; Pred. No. 1.1;
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Db 187 CTCCTAGTTTATTAGGATTGATCG 212

RESULT 7
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LOCUS      CK959074      300 bp      mRNA      linear      EST 15-MAR-2004
DEFINITION 409657 BARC 10BOV Bos taurus cDNA clone 10BOV6_A24 3', mRNA
sequence.
ACCESSION  CK959074
VERSION    CK959074.1 GI:45473454
KEYWORDS   Bos taurus (cow)
SOURCE     Bos taurus
ORGANISM   Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE  1 (bases 1 to 300)
AUTHORS   Sonstegard, T.S., Van Tassel, C.P., Matukumalli, L.K., Harhay,
G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.
TITLE     Production of EST from cDNA libraries derived from immunologically
activated bovine gut
JOURNAL    Unpublished (2004)
COMMENT   Contact: Tad S. Sonstegard
Bovine Functional Genomics Laboratory
Animal and Natural Resources Institute
Bldg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA
Tel: 3015048416
Fax: 3015048414
Email: tad@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim_alt " -trim_fasta. Vector identified

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by cross match using options -minmatch 12 -minscore 12
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FEATURES

source

1..300

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 from proximal jejunums of 18 and 21 wk old steers, and
 distal ileums of 14 day old calves, proximal jejunum
 exposed to C. oncophora for 3 and 6 weeks, and distal
 ileum exposed to C. parvum for 7 days"

ORIGIN

Query Match 93.8%; Score 24.4; DB 7; Length 300;
 Best Local Similarity 96.2%; Pred. No. 1.1;
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Qy 1 CCTCCTAGTTGTTAGGATTCATCG 26

Db 275 CCTCCTAGTTGTTGGGGATTCATCG 300

RESULT 8

BM434693/c 304 bp mRNA linear EST 31-JAN-2002
 LOCUS 1R11H08 Bos taurus Reticulum #1 library Bos taurus cDNA, mRNA
 DEFINITION

sequence.

ACCESSION BM434693

VERSION BM434693.1

KEYWORDS GI:18456415

SOURCE EST.

ORGANISM Bos taurus (cow)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.

1 (bases 1 to 304)

Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Sensen, C.W.,
 Gordon, P.M.K. and Moore, S.S.

Gene Expression Profiling of the Bovine Gastrointestinal Tract

Unpublished (2002)

Contact: Dr. Stephen Moore

Beef Genomics Laboratory

Dept of AFNS, University of Alberta

410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada

Tel: 780 492 0169

Fax: 780 492 4265

Email: stephen.moore@ualberta.ca

Insert Length: 304 Std Error: 0.00

POLYA=Yes.

Location/Qualifiers

1..304

/organism="Bos taurus"

/mol_type="mRNA"

/db_xref="taxon:9913"

/tissue_type="Smooth muscle"

/cell_type="Stratified squamous epithelial"

/dev_stage="Young adult"

/lab_host="XLI-BlueMRF strain"

/clone_lib="Bos taurus Reticulum #1 library"

/note="Organ: Reticulum; Vector: Uni-2ZAPXR; Site_1:

EcorI; Site_2: Xho I"

ORIGIN

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 Best Local Similarity 96.2%; Pred. No. 1.1;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTCCTAGTTGTTAGGATTCATCG 26

Db 50 CCTCCTAGTTGTTGGGGATTCATCG 25

RESULT 9

BM434895/c

LOCUS 1R15007

Bo taurus Reticulum #1 library Bos taurus cDNA, mRNA

DEFINITION

sequence.

ACCESSION BM434895

VERSION BM434895.1

KEYWORDS GI:18456617

SOURCE EST.

ORGANISM Bos taurus (cow)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.

1 (bases 1 to 322)

Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Sensen, C.W.,
 Gordon, P.M.K. and Moore, S.S.

Gene Expression Profiling of the Bovine Gastrointestinal Tract

Unpublished (2002)

Contact: Dr. Stephen Moore

Beef Genomics Laboratory

Dept of AFNS, University of Alberta

410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada

Tel: 780 492 0169

Fax: 780 492 4265

Email: stephen.moore@ualberta.ca

Insert Length: 322 Std Error: 0.00

POLYA=No.

Location/Qualifiers

1..322

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/mol_type="mRNA"

/db_xref="taxon:9913"

/tissue_type="Smooth muscle"

/cell_type="Stratified squamous epithelial"

/dev_stage="Young adult"

/lab_host="XLI-BlueMRF strain"

/clone_lib="Bos taurus Reticulum #1 library"

/note="Organ: Reticulum; Vector: Uni-2ZAPXR; Site_1:

EcorI; Site_2: Xho I"

ORIGIN

Query Match 93.8%; Score 24.4; DB 4; Length 322;
 Best Local Similarity 96.2%; Pred. No. 1.1;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTCCTAGTTGTTAGGATTCATCG 26

Db 222 CCTCCTAGTTGTTGGGGATTCATCG 197

RESULT 10

BM434895/c

LOCUS 1R15007

Bo taurus Reticulum #1 library Bos taurus cDNA, mRNA

DEFINITION

sequence.

ACCESSION BM434895

VERSION BM434895.1

KEYWORDS GI:15379904

SOURCE EST.

ORGANISM Bos taurus (cow)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.

1 (bases 1 to 324)

AUTHORS
 Smith, T.P.L., Grosse, W.M., Preking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Perte, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J., and Keele, J.W.
TITLE
 Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle
JOURNAL
 Genome Res. 11 (4), 626-630 (2001)
MEDLINE
 21180013
PUBMED
 11282978
COMMENT
 Contact: Smith TPL
 USDA, ARS, US Meat Animal Research Center
 PO Box 166, Clay Center, NE 68933-0166, USA
 Tel: 402 762 4366
 Fax: 402 762 4390
 Email: smith@email.marc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
 PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCCTCCAGTCACGACG
 Plate: 137 row: P column: 3
 Seq primer: ATTAGTGACACTATAG.
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 /db_xref="taxon:9913"
 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="MARC 4BOV"
 /notes="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI; Library made from pooled tissue from day 20 and day 40 embryos."
ORIGIN
 Query Match 93.8%; Score 24.4; DB 4; Length 324;
 Best Local Similarity 96.2%; Pred. No. 1.1;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CCTCCTAGTTGTTAGGGATTGATCG 26
 |||||
 Db 50 CCTCCTAGTTGTTAGGGATTGATCG 25
 |||||
 RESULT 11
 AJ693580/c 328 bp mRNA linear EST 29-JUN-2004
 LOCUS
 DEFINITION
 AJ693580 KN261 Bos taurus cDNA clone KN261-041_K22, mRNA sequence.
 ACCESSION
 AJ693580
 VERSION
 AJ693580.1 GI:49426999
 KEYWORDS
 EST.
 SOURCE
 Bos taurus (cow)
 ORGANISM
 Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.
 REFERENCE
 1 (bases 1 to 328)
 Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
 Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
 Unpublished (2004)
 Contact: Anderson SI
 Genomics and Bioinformatics
 Roslin Institute
 Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
 Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options. Vector:pBlueScriptII (SK+) R. Site1: EcoRI
 R. Site2: SmaI 5'; Seq Primer T3 Normalised library constructed from bovine ovary. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,

FEATURES
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 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /clone="KN261-041_K22"
 /tissue_type="ovary"
 /clone_lib="KN261"
 /notes="Vector: pBlueScriptII (SK+); Site 1: EcoRI; Site 2: SmaI; Single pass sequencing. Normalised library constructed from bovine ovary."
ORIGIN
 Query Match 93.8%; Score 24.4; DB 1; Length 328;
 Best Local Similarity 96.2%; Pred. No. 1.1;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CCTCCTAGTTGTTAGGGATTGATCG 26
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 Db 57 CCTCCTAGTTGTTAGGGATTGATCG 32
 |||||
 RESULT 12
 BM435757/c 330 bp mRNA linear EST 31-JAN-2002
 LOCUS
 DEFINITION
 BM435757 IRU3C3.ab1 Bos taurus Rumen #1 library Bos taurus cDNA, mRNA sequence.
 ACCESSION
 BM435757
 VERSION
 BM435757.1 GI:18457479
 KEYWORDS
 EST.
 SOURCE
 Bos taurus (cow)
 ORGANISM
 Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.
 REFERENCE
 1 (bases 1 to 330)
 Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Senses, C.W., Gordon, P.M.K. and Moore, S.S.
 Gene Expression Profiling of the Bovine Gastrointestinal Tract
 Unpublished (2002)
 Contact: Dr. Stephen Moore
 Beef Genomics Laboratory
 Dept of AFNS, University of Alberta
 410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
 Tel: 780 492 0169
 Fax: 780 492 4265
 Email: stephen.moore@ualberta.ca
 Insert Length: 330 Std Error: 0.00
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 /mol_type="mRNA"
 /db_xref="taxon:9913"
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 /call_type="Stratified squamous epithelial"
 /dev_stage="young adult"
 /lab_host="XLI-BlueMRF strain"
 /clone_lib="Bos taurus Rumen #1 library"
 /notes="Organ: Rumen; Vector: Uni-ZAPXR; Site 1: EcoRI; Site 2: Xho I"
ORIGIN
 Query Match 93.8%; Score 24.4; DB 4; Length 330;
 Best Local Similarity 96.2%; Pred. No. 1.1;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 Db 62 CCTCCTAGTTGTTAGGGATTGATCG 37
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RESULT 13
 CK727400
 LOCUS UMC-bend_0A01-006-d11 Day 5 Uterus bend Bos taurus cDNA 3', mRNA
 DEFINITION
 ACCESSION CK727400
 VERSION CK727400.1 GI:42580914
 KEYWORDS EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.
 1 (bases 1 to 330)
 Prather, R.S., Antoniou, E., Garverick, H.A., Green, J.A., Lucy, M.C.,
 Roberts, R.M., Smith, M.F. and Youngquist, R.S.
 USDA Grant NRI-2002-03476: Bovine ESTs: Focus on Female
 Reproduction
 Unpublished (2002)
 Contact: DNA Core Facility
 Animal Science - RS Prather
 University of Missouri-Columbia
 M616 Medical Sciences Bldg., Columbia, MO 65212, USA
 Tel: (573)882-0428
 Fax: (573)884-5552
 Email: bovine@net.missouri.edu
 POLYA=Yes.

FEATURES

Source
 Location/Qualifiers
 1..330
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 /clone_lib="bend"
 /note="Funding: The production of ESTs submitted in this project was funded by USDA Grant NRI-2002-03476 entitled 'Bovine ESTs: Focus on Female Reproduction' to RS Prather, E Antoniou, HA Garverick, JA Green, MC Lucy, RM Roberts, MF Smith and RS Youngquist. Genetic Source: Heifers for the project were purchased from Circle A Ranch, Iberia, MO (http://www.circlearanch.com/home.html). These heifers, while not registered have known Angus pedigrees going back at least 4 generations. Samples collected: The samples consisted of the following: germinal vesicle-stage oocytes; in vitro derived embryos (2-cell, morula, blastocyst and nuclear transfer blastocyst); in vivo corpora lutea (days 3, 5, 8, 14, 16, 18 and 35); ovarian follicles (days 0, non-recruited, recruited, early selected and preovulatory); oviduct (days 0, 3 and 5); endometrium (days 5, 8, 14, 16, 18 and 35); and placenta/embryo from day 35 conceptuses. Expanded descriptions of how the tissues were collected can be found at the following URL: http://genome.net.missouri.edu/Bovine/Methods.html. Library construction (Standard Protocol): All procedures have been described in detail elsewhere (Soares et al., 1994; Bonaldo et al., 1996; Jiang et al., 2001). Total cellular RNA from each sample was isolated by using STAT-60 reagent (Tel-Test, Friendswood, TX) and the poly(A)+ RNA was obtained by two rounds of purification with the Oligotex mRNA isolation kit (Qiagen) according to the manufacturer's instructions. The libraries were constructed by E. Ferguson and R. Woods essentially as described by the manufacturer's instructions provided with the SuperScript Plasmid System (Invitrogen, cat. no. 18248-013). Briefly, 1mcg of poly(A)+ RNA was annealed at c37 degrees with 10mcg of NotI-tag-drl8 oligonucleotide (GCGTCGCGCGCG-tag-T18) and reverse transcribed at c37 degrees with SuperScript II (Invitrogen) reverse transcriptase (Jiang et al., 2001). The 'tag' represents a tissue/stage-specific ten-base sequence identifier (http://genome.uiowa.edu/pubsoft/software.html) present in the oligonucleotide used to prime first-strand synthesis.

Second strand synthesis was performed with T4 DNA polymerase in the presence of DNA ligase and RNase H. After second strand synthesis, the double-stranded cDNAs were ligated to SalI adapters (Invitrogen-Life Technologies) and digested with NotI. The cDNAs were size selected by passage through cDNA size fractionation columns (Invitrogen-Life Technologies). The cDNAs derived from each developmental stage of a particular tissue were mixed on an equimolar basis and ligated directionally into the NotI and SalI sites of the pCMV-SPORT6 vector (Invitrogen). After ligation of the inserts, the plasmids were electroporated into DH10B bacteria. Library Construction (PCR protocol): The amount of mRNA that was recovered from oocytes and embryos was quite limiting and was not sufficient for library production with the standard protocol. Therefore, PCR-based protocol was utilized for producing libraries from sources in which the amount of extracted mRNA was small (oocytes and embryos). Poly-A RNA was isolated by using the MicroPoly(A) Pure kit from Ambion (cat. # 1918). The mRNA was reverse transcribed with a NotI-tag-drl8 oligonucleotide and a SMART oligonucleotide (Clontech) modified to contain a SalI site to generate full-length cDNA with a sequence complementary to the SMART oligonucleotide. Sequences within the SMART and dr oligonucleotides were used as primers to amplify the cDNAs by PCR with pfu turbo polymerase (Stratagene). The resulting PCR products were purified, digested with NotI and SalI and size fractionated by using Chroma Spin-1000 columns (Clontech). Purified cDNA from each PCR reaction was quantitated and mixed on an equimolar basis for ligation into the pCMV-SPORT6 vector. Preliminary Library Characterization: Randomly chosen clones from each library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (~4 96-well plates) to confirm library quality [e.g. the presence of short polyA+ tails, genomic DNA contamination (must be <1%), ribosomal RNA clones (must be <1%), etc.] and to provide a sequence database representing the predominant clones in each library. The clones were sequenced at the University of Missouri-Columbia DNA Core Facility. After production of the libraries, equal numbers of recombinants from each library were pooled to produce a single mixed library (mega-library) for more extensive sequencing. Bioinformatics work was performed by GK Springer's bioinformatics group (Spollen WG, Topinka CM, Khambati AA) in Computer Science at the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri DNA Core facility at: bovine@net.missouri.edu. Bonaldo MF, Lennon G, Soares MB. Normalization and Subtraction: Two approaches to facilitate gene discovery. Genome Res, 1996; 6:791-806. Jiang H, Bivens NJ, Ries JE, Whitworth RM, Green JA, Forrester LJ, Springer GK, Didion BA, Mathialagan N, Prather RS, Lucy MC (2001) Constructing cDNA libraries with fewer clones that contain long poly(dA) tails. Biotechniques 31:38-42. Soares MB, MF Bonaldo, p Jelene, L Su, L Lawton, A Efstratiadis. 1994. Construction and characterization of a normalized cDNA library. Proc Natl Acad Sci, 91:9228-9232. TAG_TISSUE=Day 5 Uterus TAG_SEQ=ATAAGATAAC"

ORIGIN

Query Match 93.8%; Score 24.4; DB 7; Length 330;
 Best Local Similarity 96.2%; Pred. No. 1.1;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 CCTCCTAGTTTGTAGGGATTGATCG 26
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 Db 276 CCTCCTAGTTTGTAGGGATTGATCG 301
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RESULT 14
BE487585/c 331 bp mRNA linear EST 27-MAR-2003
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BE487585 331 bp mRNA linear EST 27-MAR-2003
BE487585
BE487585.1 GI:9607118
EST.
Bos taurus (cow)
Bos taurus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 331)
Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P.,
Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
and Quackenbush, J.
Analysis of bovine mammary gland EST and functional annotation of
the Bos taurus gene index
Mamm. Genome 13 (7), 373-379 (2002)
22135956
12140684
Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414
Email: tads@psi.barc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCACGTCACGACG
Plate: 138 row: 6 column: 9
Seq primer: ATTAGGTGACACTATAG.
Location/Qualifiers
1. .331
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/lab_host="DH10B"
/clone_lib="BARC 5BOV"
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."

ORIGIN
Query Match 93.8%; Score 24.4; DB 2; Length 331;
Best Local Similarity 96.2%; Pred. No. 1.1; Indels 0; Gaps 0;
Matches 25; Conservative 0; Mismatches 1;
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RESULT 15
CN998120
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CN998120 331 bp mRNA linear EST 09-JUN-2004
UMC-bcl1 OA02-003-e08 Day 16 Corpus luteum from a pregnant animal
bcl1 Bos taurus cDNA 3', mRNA sequence.
CN998120
CN998120.1 GI:48490010
EST.
Bos taurus (cow)
Bos taurus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 331)
Prather, R.S., Antoniou, E., Garverick, H.A., Green, J.A., Lucy, M.C.,

Roberts, R.M., Smith, M.F. and Youngquist, R.S.
USDA Grant NRI-2002-03476: Bovine ESTs: Focus on Female
Reproduction
Unpublished (2002)
Contact: DNA Core Facility
Animal Science - RS Prather
University of Missouri-Columbia
M616 Medical Sciences Bldg., Columbia, MO 65212, USA
Tel: (573) 882-0428
Fax: (573) 884-5552
Email: bovine@rnet.missouri.edu
POLYA=Yes.
Location/Qualifiers
1. .331
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone_lib="bcl1"
/notes="Funding: The production of ESTs submitted in this
project was funded by USDA Grant NRI-2002-03476 entitled
'Bovine ESTs: Focus on Female Reproduction' to RS
Prather (Primary Investigator), E Antoniou, HA Garverick,
JA Green, MC Lucy, RM Roberts, MF Smith and RS Youngquist.
Genetic Source: Heifers for the project were purchased
from Circle A Ranch, Iberia, MO
(http://www.circlearanch.com/home.html). These heifers,
while not registered have known Angus pedigrees going back
at least 4 generations. Samples collected: The samples
consisted of the following: germinal vesicle-stage
oocytes; in vitro derived embryos (2-cell, morula,
blastocyst and nuclear transfer blastocyst); in vivo
corpora lutea (days 3, 5, 8, 14, 16, 18 and 35); ovarian
follicles (days 0, non-recruited, recruited, early
selected and preovulatory); oviduct (days 0, 3 and 5);
endometrium (days 5, 8, 14, 16, 18 and 35); and
placenta/embryo from day 35 conceptuses. Expanded
descriptions of how the tissues were collected can be
found at the following URL:
http://genome.rnet.missouri.edu/Bovine/Methods.html.
Library construction (Standard Protocol): All procedures
have been described in detail elsewhere (Soares et al.,
1994; Bonaldo et al., 1996; Jiang et al., 2001). Total
cellular RNA from each sample was isolated by using
STAT-60 reagent (Tel-Test, Friendswood, TX) and the
poly(A)+ RNA was obtained by two rounds of purification
with the Oligotex mRNA isolation kit (Qiagen) according to
the manufacturer's instructions. The libraries were
constructed essentially as described by the manufacturer's
instructions provided with the SuperScript plasmid system
(Invitrogen, cat. no. 18248-013). Briefly, 1mcg of
poly(A)+ RNA was annealed at c37 degrees with 10mcg of
NotI-tag-dT18 oligonucleotide (GCTGCTCGCGCGC-tag-T18)
and reverse transcribed at c37 degrees with SuperScript II
(Invitrogen) reverse transcriptase (Jiang et al., 2001).
The 'tag' represents a tissue/stage-specific ten-base
sequence identifier
(http://genome.ualowa.edu/pubsoft/software.html) present in
the oligonucleotide used to prime first-strand synthesis.
Second strand synthesis was performed with T4 DNA
polymerase in the presence of DNA ligase and RNase H.
After second strand synthesis, the double-stranded cDNAs
were ligated to SalI adapters (Invitrogen-Life
Technologies) and digested with NotI. The cDNAs were size
selected by passage through cDNA size fractionation
columns (Invitrogen-Life Technologies). The cDNAs derived
from each developmental stage of a particular tissue were
mixed on an equimolar basis and ligated directionally into
the NotI and SalI sites of the pCMV-SPORT6 vector
(Invitrogen). After ligation of the inserts, the plasmids
were electroporated into DH10B bacteria. Library
construction (PCR Protocol): The amount of mRNA that was
recovered from oocytes and embryos was quite limiting and

was not sufficient for library production with the standard protocol. Therefore, PCR-based protocol was utilized for producing libraries from sources in which the amount of extracted mRNA was small (oocytes and embryos). Poly-A RNA was isolated by using the MicroPoly(A) Pure kit from Ambion (cat. # 1918). The mRNA was reverse transcribed with a NotI-tag-dT18 oligonucleotide and a SMART oligonucleotide (Clontech) modified to contain a SalI site to generate full-length cDNA with a sequence complementary to the SMART oligonucleotide. Sequences within the SMART and dT oligonucleotides were used as primers to amplify the cDNAs by PCR with pfu turbo polymerase (Stratagene). The resulting PCR products were purified, digested with NotI and SalI and size fractionated by using Chroma Spin-1000 columns (Clontech). Purified cDNA from each PCR reaction was quantitated and mixed on an equimolar basis for ligation into the pCMV-SPORT6 vector. Preliminary Library Characterization: Randomly chosen clones from each library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (-4 96-well plates) to confirm library quality (e.g. the presence of short polyA+ tails, genomic DNA contamination (must be <1%), ribosomal RNA clones (must be <1%), etc.) and to provide a sequence database representing the predominant clones in each library. The clones were sequenced at the University of Missouri-Columbia DNA Core Facility. After production of the libraries, equal numbers of recombinants from each library were pooled to produce a single mixed library (mega-library) for more extensive sequencing.

Bioinformatics work was performed by GK Springer's Bioinformatics group in Computer Science at the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri DNA Core facility at: bovine@net.missouri.edu. Bonaldo MF, Lennon G, Soares MB. Normalization and Subtraction: Two approaches to facilitate gene discovery. Genome Res, 1996; 6:791-806. Jiang H, Bivens NJ, Ries JE, Whitworth KM, Green JA, Forrester LJ, Springer GK, Didion EA, Mathialagan N, Prather RS, Lucy MC (2001) Constructing cDNA libraries with fewer clones that contain long poly(dA) tails. Biotechniques 31:38-42. Soares MB, MF Bonaldo, P Jelene, L Su, L Lawton, A Efstratiadis. 1994. Construction and characterization of a normalized cDNA library. Proc Natl Acad Sci, 91:9228-9232. TAG_TISSUE=Day 16 Corpus luteum from a pregnant animal TAG_SEQ=CTGCTAGTAG"

ORIGIN

Query Match	93.8%;	Score 24.4;	DB 7;	Length 331;
Best Local Similarity	96.2%;	Pred. No. 1.1;		
Matches 25;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;

Qy	1	CCTCCTAGTTTCTAGGGATTGATCG	26
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Search completed: November 17, 2004, 02:10:51
Job time : 361.388 secs


```
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; SEQ ID NO 3962
; LENGTH: 235
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 17-LIB34-051-Q1-E1-E1
US-09-960-352-3962

Query Match      93.8%; Score 24.4; DB 9; Length 235;
Best Local Similarity 96.2%; Pred. No. 0.21;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTGTTAGGGATTGATCG 26
Db 144 CCTCCTAGTTGTTAGGGATTGATCG 119

RESULT 3
US-09-960-352-5417/c
; Sequence 5417, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; SEQ ID NO 5417
; LENGTH: 241
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 23-LIB34-052-Q1-E1-F3
US-09-960-352-5417

Query Match      93.8%; Score 24.4; DB 9; Length 241;
Best Local Similarity 96.2%; Pred. No. 0.21;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTGTTAGGGATTGATCG 26
Db 96 CCTCCTAGTTGTTAGGGATTGATCG 71

RESULT 4
US-09-960-352-3998/c
; Sequence 3998, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
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; SEQ ID NO 3998
; LENGTH: 331
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 17-LIB34-084-Q1-E1-E9
US-09-960-352-3998

Query Match      93.8%; Score 24.4; DB 9; Length 331;
Best Local Similarity 96.2%; Pred. No. 0.22;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTGTTAGGGATTGATCG 26
Db 78 CCTCCTAGTTGTTAGGGATTGATCG 53

RESULT 5
US-09-960-352-12066/c
; Sequence 12066, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 12066
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 52-BOVMS1-008-Q1-E1-E8
US-09-960-352-12066

Query Match      93.8%; Score 24.4; DB 9; Length 411;
Best Local Similarity 96.2%; Pred. No. 0.23;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTGTTAGGGATTGATCG 26
Db 135 CCTCCTAGTTGTTAGGGATTGATCG 110

RESULT 6
US-09-960-352-9213/c
; Sequence 9213, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 9213
; LENGTH: 416
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 40-BOVMS1-002-Q1-E1-B8
US-09-960-352-9213

Query Match      93.8%; Score 24.4; DB 9; Length 416;
Best Local Similarity 96.2%; Pred. No. 0.23;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 CCTCCTAGTTTGTAGGATTGATCG 26
Db 115 CCTCCTAGTTTGTGGGATTGATCG 90

RESULT 7
US-09-960-352-13007/c
; Sequence 13007, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 13007
; LENGTH: 417
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 56-BOVMS1-006-Q1-E1-F12
US-09-960-352-13007

Query Match 93.8%; Score 24.4; DB 9; Length 417;
Best Local Similarity 96.2%; Pred. No. 0.23;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTTGTAGGATTGATCG 26
Db 152 CCTCCTAGTTTGTGGGATTGATCG 127

RESULT 8
US-09-960-352-2332/c
; Sequence 2332, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 2332
; LENGTH: 419
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 11-BOVMS1-005-Q1-E1-C3
US-09-960-352-2332

Query Match 93.8%; Score 24.4; DB 9; Length 419;
Best Local Similarity 96.2%; Pred. No. 0.23;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTTGTAGGATTGATCG 26
Db 194 CCTCCTAGTTTGTGGGATTGATCG 169

RESULT 9
US-09-960-352-8757/c
; Sequence 8757, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 8757
; LENGTH: 448
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 38-BOVMS1-021-Q1-E1-B6
US-09-960-352-8757

Query Match 93.8%; Score 24.4; DB 9; Length 448;
Best Local Similarity 96.2%; Pred. No. 0.23;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTTGTAGGATTGATCG 26
Db 404 CCTCCTAGTTTGTGGGATTGATCG 379

RESULT 10
US-09-960-352-1158/c
; Sequence 1158, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 1158
; LENGTH: 469
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (422)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 06-BOVMS1-014-Q1-E1-B5
US-09-960-352-1158

Query Match 93.8%; Score 24.4; DB 9; Length 469;
Best Local Similarity 96.2%; Pred. No. 0.23;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTTGTAGGATTGATCG 26
Db 378 CCTCCTAGTTTGTGGGATTGATCG 353

RESULT 11
US-09-960-352-5211/c
; Sequence 5211, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
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; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 5211
; LENGTH: 475
; TYPE: DNA
; ORGANISM: Bos taurus
; NAME/KEY: unsure
; FEATURE:
; LOCATION: (7)..(423)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 23-BOWNS1-009-Q1-E1-F11
US-09-960-352-5211

Query Match 93.8%; Score 24.4; DB 9; Length 475;
Best Local Similarity 96.2%; Pred. No. 0.23;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTCCTAGTTTGTAGGATTGATCG 26
Db 379 CCTCCTAGTTTGTGGGATTGATCG 354

RESULT 12

US-09-876-143-1164/c
; Sequence 1164, Application US/09876143
; Publication No. US20040081958A1
; GENERAL INFORMATION:
; APPLICANT: Infogen Inc.
; APPLICANT: EILERTSEN, KENNETH J.
; APPLICANT: PFISTER-GENSKOW, MARTHA
; APPLICANT: CHILDS, LYNETTE
; APPLICANT: FORSYTHE, TODD
; APPLICANT: BISHOP, MICHAEL D.
; TITLE OF INVENTION: IDENTIFICATION AND USE OF MOLECULAR MARKERS INDICATING
; FILE REFERENCE: 028040-0202
; CURRENT APPLICATION NUMBER: US/09/876,143
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 60/209,874
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 1744
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1164
; LENGTH: 979
; TYPE: DNA
; ORGANISM: Bovine
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(979)
; OTHER INFORMATION: n is a, c, g, or t
US-09-876-143-1164

Query Match 93.8%; Score 24.4; DB 11; Length 979;
Best Local Similarity 96.2%; Pred. No. 0.26;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCTCCTAGTTTGTAGGATTGATCG 26
Db 192 CCTCCTAGTTTGTGGGATTGATCG 167

RESULT 13

US-10-242-535A-44171/c
; Sequence 44171, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783

; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44171
; LENGTH: 120
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-44171

Query Match 87.7%; Score 22.8; DB 16; Length 120;
Best Local Similarity 92.3%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCTCCTAGTTTGTAGGATTGATCG 26
Db 59 CCTCCTAGTTTGTAGGACGATCG 34

RESULT 14

US-10-085-783A-44171/c
; Sequence 44171, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44171
; LENGTH: 120
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-44171

Query Match 87.7%; Score 22.8; DB 16; Length 120;
Best Local Similarity 92.3%; Pred. No. 1;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCTCCTAGTTTGTAGGATTGATCG 26
Db 59 CCTCCTAGTTTGTAGGACGATCG 34

RESULT 15

US-09-878-178-824
; Sequence 824, Application US/09878178
; Patent No. US20020177552A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.527
; CURRENT APPLICATION NUMBER: US/09/878,178
; CURRENT FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 2237
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 824
; LENGTH: 231
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(231)
; OTHER INFORMATION: n = A,T,C or G
US-09-878-178-824
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Query Match      87.7%; Score 22.8; DB 9; Length 231;
Best Local Similarity 92.3%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy      1 CCTCCTAGTTTGTAGGGATTGATCG 26
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Db      199 CCTCCTAGTTTGTAGGGACGATCG 224
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 23:55:00 ; Search time 9.24665 Seconds
(without alignments)
1998.616 Million cell updates/sec

Title: US-09-821-782E-2

Perfect score: 26

Sequence: 1 cctcctagttttagggattgatcg 26

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22.8	87.7	578	3	US-09-328-111-763
2	22.8	87.7	591	3	US-09-385-982-493
3	22.8	87.7	597	3	US-09-328-111-562
4	22.8	87.7	619	3	US-09-385-982-510
5	22.8	87.7	668	3	US-09-328-111-812
6	22.8	87.7	1140	4	US-09-377-497-7
7	22.8	87.7	16568	4	US-09-525-906-1
8	22.8	87.7	16569	3	US-09-097-889-2
9	22.8	87.7	16569	3	US-09-377-856-1
10	22.8	87.7	16569	4	US-09-302-681-2
11	22.8	87.7	16569	4	US-09-098-079-2
12	22.8	87.7	16569	4	US-10-053-611-1
13	21.2	81.5	30	1	US-08-647-584-46
14	21.2	81.5	602	3	US-09-385-982-375
15	20.8	80.0	315	4	US-09-313-294A-7516
16	18	69.2	99629	4	US-09-596-002-37
17	17.8	68.5	638	4	US-09-621-976-3609
18	17.6	67.7	616	4	US-09-270-767-31042
19	17.6	67.7	709	4	US-09-270-767-14799
20	17.2	66.2	12141	3	US-09-488-671-10
21	17	65.4	349	4	US-09-621-976-10857
22	17	65.4	447	4	US-09-107-532A-404
23	17	65.4	2242	4	US-09-738-946-9
24	16.8	64.6	21	1	US-08-647-584-107
25	16.6	63.8	472	4	US-09-513-999C-22922
26	16.6	63.8	618	3	US-09-385-982-200
27	16.6	63.8	720	1	US-08-153-848-35

C 28 16.6 63.8 720 3 US-09-299-843A-35 Sequence 35, Appl
C 29 16.6 63.8 720 3 US-09-088-337B-35 Sequence 35, Appl
C 30 16.6 63.8 720 5 PCT-US93-11153-35 Sequence 35, Appl
C 31 16.6 63.8 1034 4 US-09-270-767-12161 Sequence 1, Appl
C 32 16.6 63.8 2841 2 US-08-452-075-1 Sequence 1, Appl
C 33 16.6 63.8 2841 3 US-09-231-061-1 Sequence 1, Appl
C 34 16.6 63.8 2841 3 US-09-011-762-5 Sequence 5, Appl
C 35 16.6 63.1 2091 4 US-09-107-532A-2479 Sequence 2479, Ap
C 36 16.2 62.3 786 4 US-09-328-352-2493 Sequence 2493, Ap
C 37 16.2 62.3 1014 3 US-09-134-001C-370 Sequence 370, Ap
C 38 16.2 62.3 1692 4 US-09-107-532A-3287 Sequence 3287, Ap
C 39 16.2 62.3 1884 1 US-08-307-382-3 Sequence 3, Appl
C 40 16.2 62.3 1884 1 US-08-366-779-3 Sequence 3, Appl
C 41 16.2 62.3 1884 1 US-08-478-727-3 Sequence 3, Appl
C 42 16.2 62.3 1884 1 US-08-473-508-3 Sequence 3, Appl
C 43 16.2 62.3 1884 1 US-08-789-936-3 Sequence 3, Appl
C 44 16.2 62.3 1884 3 US-08-934-254-3 Sequence 3, Appl
C 45 16.2 62.3 1884 4 US-09-685-775-3 Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-09-328-111-763
; Sequence 763, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
; APPLICANT: Endege, Wilson O.
; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Derti, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/328,111
; CURRENT FILING DATE: 1999-06-08
; EARLIER FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 763
; LENGTH: 578
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(578)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-111-763

Query Match 87.7%; Score 22.8; DB 3; Length 578;
Best Local Similarity 92.3%; Pred. No. 0.054;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCTCCTAGTTTGTAGGATGATCG 26
|||
Db 305 CCTCCTAGTTTGTAGGACGATCG 330

RESULT 2
US-09-385-982-493
; Sequence 493, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:

; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCNA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; CURRENT FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 493
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(591)
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-493

Query Match 87.7%; Score 22.8; DB 3; Length 591;
Best Local Similarity 92.3%; Pred. No. 0.054;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTTGTAGGATTCATCG 26
Db 199 CCTCCTAGTTTGTAGGACGGATCG 224

RESULT 3

US-09-328-111-562
; Sequence 562, Application US/09328111
; Patent No. 6262333

; GENERAL INFORMATION:
; APPLICANT: Endege, Wilson O.
; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Derti, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/328,111
; CURRENT FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: US 60/088,801
; EARLIER FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 562
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(597)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-111-562

Query Match 87.7%; Score 22.8; DB 3; Length 597;
Best Local Similarity 92.3%; Pred. No. 0.054;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTTGTAGGATTCATCG 26
Db 205 CCTCCTAGTTTGTAGGACGGATCG 230

RESULT 4

US-09-385-982-510
; Sequence 510, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCNA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; CURRENT FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 510
; LENGTH: 619
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(619)
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-510

Query Match 87.7%; Score 22.8; DB 3; Length 619;
Best Local Similarity 92.3%; Pred. No. 0.054;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTTGTAGGATTCATCG 26
Db 199 CCTCCTAGTTTGTAGGACGGATCG 224

RESULT 5

US-09-328-111-812
; Sequence 812, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
; APPLICANT: Endege, Wilson O.
; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Derti, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/328,111
; CURRENT FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: US 60/088,801
; EARLIER FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 812
; LENGTH: 668
; TYPE: DNA
; ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(668)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-111-812

Query Match      87.7%; Score 22.8; DB 3; Length 668;
Best Local Similarity 92.3%; Pred. No. 0.055; 2; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTCCTAGTTTCTTAGGGATTGATCG 26
   |||||
Db 199 CCTCCTAGTTTCTTAGGGACGGATCG 224
   |||||

RESULT 6
US-09-377-497-7/c
; Sequence 7, Application US/09377497
; Patent No. 6670119
; GENERAL INFORMATION:
; APPLICANT: YOSHIKAWA, YOSHIE
; APPLICANT: MUKAI, HIROYUKI
; APPLICANT: ASADA, KIYOZO
; APPLICANT: HINO, FUMITSUGU
; APPLICANT: KATO, IKUNOSHIN
; TITLE OF INVENTION: CANCER-ASSOCIATED GENES
; FILE REFERENCE: 1422-388P
; CURRENT APPLICATION NUMBER: US/09/377,497
; CURRENT FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: any n or Xaa = unknown
US-09-377-497-7

Query Match      87.7%; Score 22.8; DB 4; Length 1140;
Best Local Similarity 92.3%; Pred. No. 0.061; 2; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTCCTAGTTTCTTAGGGATTGATCG 26
   |||||
Db 869 CCTCCTAGTTTCTTAGGGACGGATCG 844
   |||||

RESULT 7
US-09-525-906-1/c
; Sequence 1, Application US/09525906
; Patent No. 6605433
; GENERAL INFORMATION:
; APPLICANT: Jen, Jen
; APPLICANT: Sidransky, David
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Fliss, Makiko
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: Mitochondrial Dosimeter
; FILE REFERENCE: 1107.85815
; CURRENT APPLICATION NUMBER: US/09/525,906
; CURRENT FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 09/377,856
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: 60/097,307
; PRIOR FILING DATE: 1998-08-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 16568
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-09-525-906-1
Query Match      87.7%; Score 22.8; DB 4; Length 16568;
Best Local Similarity 92.3%; Pred. No. 0.1; 2; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTCCTAGTTTCTTAGGGATTGATCG 26
   |||||
Db 15614 CCTCCTAGTTTCTTAGGGACGGATCG 15589
   |||||

RESULT 8
US-09-097-889-2/c
; Sequence 2, Application US/09097889
; Patent No. 6218117
; GENERAL INFORMATION:
; APPLICANT: Herrnstadt, Corrina
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
; TITLE OF INVENTION: AGENTS THAT QUANTITATIVELY ALTER DETECTABLE
; TITLE OF INVENTION: EXTRAMITOCHONDRIAL DNA: MITOCHONDRIAL DNA RATIOS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/097,889
; FILING DATE: 15-JUN-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenman Ph.D., Stephen J.
; REGISTRATION NUMBER: 43,058
; REFERENCE/DOCKET NUMBER: 660088.417
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16569 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-097-889-2

Query Match      87.7%; Score 22.8; DB 3; Length 16569;
Best Local Similarity 92.3%; Pred. No. 0.1; 2; Indels 0; Gaps 0;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CTCCTAGTTTCTTAGGGATTGATCG 26
   |||||
Db 15615 CCTCCTAGTTTCTTAGGGACGGATCG 15590
   |||||

RESULT 9
US-09-377-856-1/c
; Sequence 1, Application US/09377856
; Patent No. 6344322
; GENERAL INFORMATION:
; APPLICANT: Polyak, Kornelia
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: Subtle Mitochondrial Mutations as Tumor
; TITLE OF INVENTION: Markers
```

```
; FILE REFERENCE: 1107.82346
; CURRENT APPLICATION NUMBER: US/09/377,856
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: 60/097,307
; PRIOR FILING DATE: 1998-08-20
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 16569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-377-856-1

Query Match      87.7%; Score 22.8; DB 3; Length 16569;
Best Local Similarity 92.3%; Pred. No. 0.1;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTTGTAGGGATTGATCG 26
Db 15615 CCTCCTAGTTTGTAGGGACGGATCG 15590

RESULT 10
US-09-302-681-2/c
; Sequence 2, Application US/09302681
; Patent No. 6441149
; GENERAL INFORMATION:
; APPLICANT: Herrnstadt, Corrina
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Clevenger, William
; APPLICANT: Fahy, Eoin F.
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: QUANTIFICATION OF EXTRAMITOCHONDRIAL DNA
; FILE REFERENCE: 660088.416C1
; CURRENT APPLICATION NUMBER: US/09/302,681
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 16569
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-302-681-2

Query Match      87.7%; Score 22.8; DB 4; Length 16569;
Best Local Similarity 92.3%; Pred. No. 0.1;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTTGTAGGGATTGATCG 26
Db 15615 CCTCCTAGTTTGTAGGGACGGATCG 15590

RESULT 11
US-09-098-079-2/c
; Sequence 2, Application US/09098079
; Patent No. 6489095
; GENERAL INFORMATION:
; APPLICANT: Herrnstadt, Corrina
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Clevenger, William
; APPLICANT: Fahy, Eoin F.
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: DIAGNOSTIC METHOD BASED ON QUANTIFICATION OF
; TITLE OF INVENTION: EXTRAMITOCHONDRIAL DNA
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
```

```
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/098,079
; FILING DATE: 15-JUN-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenman Ph.D., Stephen J.
; REGISTRATION NUMBER: 43,058
; REFERENCE/DOCKET NUMBER: 660088.416
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16569 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-098-079-2

Query Match      87.7%; Score 22.8; DB 4; Length 16569;
Best Local Similarity 92.3%; Pred. No. 0.1;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTTGTAGGGATTGATCG 26
Db 15615 CCTCCTAGTTTGTAGGGACGGATCG 15590

RESULT 12
US-10-053-611-1/c
; Sequence 1, Application US/10053611
; Patent No. 6750021
; GENERAL INFORMATION:
; APPLICANT: Polyak, Kornelia
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: Subtle Mitochondrial Mutations as Tumor
; TITLE OF INVENTION: Markers
; FILE REFERENCE: 1107.82346
; CURRENT APPLICATION NUMBER: US/10/053,611
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US/09/377,856
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: 60/097,307
; PRIOR FILING DATE: 1998-08-20
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 16569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-053-611-1

Query Match      87.7%; Score 22.8; DB 4; Length 16569;
Best Local Similarity 92.3%; Pred. No. 0.1;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTTGTAGGGATTGATCG 26
Db 15615 CCTCCTAGTTTGTAGGGACGGATCG 15590

RESULT 13
US-08-647-584-46/c
; Sequence 46, Application US/08647584
; Patent No. 5786144
; GENERAL INFORMATION:
```

APPLICANT: De Salle, Rob
APPLICANT: Birstein, Vadim J.
TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR
IDENTIFICATION OF SPECIES ORIGIN OF CAVIAR
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
ADDRESSEE: Weil, Gotshal & Manges LLP
STREET: 2882 Sand Hill Road, Suite 280
CITY: Menlo Park
STATE: California
COUNTRY: U.S.A.
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/647,584
FILING DATE: 13-MAY-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Baran, Alexandra J.
REGISTRATION NUMBER: 39,101
REFERENCE/DOCKET NUMBER: 14503.4010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 926-6200
TELEFAX: (415) 854-3713
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-647-584-46

Query Match 81.5%; Score 21.2; DB 1; Length 30;
Best Local Similarity 88.5%; Pred. No. 0.19;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCTCCTAGTTTGTAGGGATTGATCG 26
Db 26 CCGCCTAGTTTGTAGGGATTGATCG 1

RESULT 14

US-09-385-982-375
Sequence 375, Application US/09385982
Patent No. 6262334
GENERAL INFORMATION:
APPLICANT: ENDEGE, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
FILE REFERENCE: CCDA-260XX
CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-30
EARLIER APPLICATION NUMBER: 09/328,111
EARLIER FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: 60/117,393
EARLIER FILING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: 60/098,639
EARLIER FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 544
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 375
LENGTH: 602
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(602)
OTHER INFORMATION: n = A,T,C or G

US-09-385-982-375

Query Match 81.5%; Score 21.2; DB 3; Length 602;
Best Local Similarity 88.5%; Pred. No. 0.33;
Matches 23; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCTCCTAGTTTGTAGGGATTGATCG 26
Db 199 CTTCTAGCTTGTAGGGACGGATCG 224

RESULT 15

US-09-313-294A-7516/c
Sequence 7516, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, Bradley K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 7516
LENGTH: 315
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700381866H1
NAME/KEY: unsure
LOCATION: 32, 56, 84, 87, 117-118, 160, 196, 244
OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-7516

Query Match 80.0%; Score 20.8; DB 4; Length 315;
Best Local Similarity 84.6%; Pred. No. 0.46;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCTCCTAGTTTGTAGGGATTGATCG 26
Db 119 CTTCTAGCTTGTAGGGACGGATCG 94

Search completed: November 17, 2004, 03:15:11
Job time : 11.2467 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 16:25:24 ; Search time 40.7744 Seconds
(without alignments)
3218.578 Million cell updates/sec

Title: US-09-821-782E-1

Perfect score: 25

Sequence: 1 taccatgaggacaataatcattctg 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

N_Geneseq_23Sep04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	8	ABQ83297 Cytochrom
2	25	100.0	329	8	ABX49123 Bovine ES
3	25	100.0	346	8	ABX41392 Bovine ES
4	25	100.0	353	8	ABX41185 Bovine ES
5	25	100.0	380	8	ABX42082 Bovine ES
6	25	100.0	388	8	ABX36231 Bovine ES
7	25	100.0	397	8	ABX42640 Bovine ES
8	25	100.0	402	8	ABX47053 Bovine ES
9	25	100.0	409	8	ABX44209 Bovine ES
10	25	100.0	409	8	ABX42249 Bovine ES
11	25	100.0	409	8	ABX39507 Bovine ES
12	25	100.0	411	8	ABX43333 Bovine ES
13	25	100.0	412	8	ABX35955 Bovine ES
14	25	100.0	413	8	ABX37092 Bovine ES
15	25	100.0	414	8	ABX46099 Bovine ES
16	25	100.0	415	8	ABX40021 Bovine ES
17	25	100.0	417	8	ABX41849 Bovine ES
18	25	100.0	417	8	ABX45538 Bovine ES
19	25	100.0	419	8	ABX37811 Bovine ES
20	25	100.0	420	8	ABX44580 Bovine ES
21	25	100.0	420	8	ABX35249 Bovine ES

22	25	100.0	421	8	ABX39415	Abx39415 Bovine ES
23	25	100.0	422	8	ABX47816	Abx47816 Bovine ES
24	25	100.0	424	8	ABX39981	Abx39981 Bovine ES
25	25	100.0	425	8	ABX44677	Abx44677 Bovine ES
26	25	100.0	428	8	ABX40056	Abx40056 Bovine ES
27	25	100.0	429	8	ABX46840	Abx46840 Bovine ES
28	25	100.0	432	8	ABX42116	Abx42116 Bovine ES
29	25	100.0	433	8	ABX47629	Abx47629 Bovine ES
30	25	100.0	435	8	ABX44491	Abx44491 Bovine ES
31	25	100.0	436	8	ABX36609	Abx36609 Bovine ES
32	25	100.0	443	8	ABX43069	Abx43069 Bovine ES
33	25	100.0	444	8	ABX40780	Abx40780 Bovine ES
34	25	100.0	445	8	ABX44982	Abx44982 Bovine ES
35	25	100.0	446	8	ABX47632	Abx47632 Bovine ES
36	25	100.0	446	8	ABX48097	Abx48097 Bovine ES
37	25	100.0	447	8	ABX39586	Abx39586 Bovine ES
38	25	100.0	447	8	ABX38849	Abx38849 Bovine ES
39	25	100.0	448	8	ABX37805	Abx37805 Bovine ES
40	25	100.0	455	8	ABX38792	Abx38792 Bovine ES
41	25	100.0	458	8	ABX38588	Abx38588 Bovine ES
42	25	100.0	472	8	ABQ83339	Abq83339 Mitochond
43	25	100.0	472	8	ABQ83321	Abq83321 Mitochond
44	25	100.0	472	8	ABQ83322	Abq83322 Mitochond
45	25	100.0	472	8	ABQ83332	Abq83332 Mitochond

ALIGNMENTS

RESULT 1

ABQ83297

ID ABQ83297 standard; DNA; 25 BP.

XX

AC ABQ83297;

XX

DT 18-JAN-2003 (first entry)

XX

DE Cytochrome b gene universal PCR primer mcb 398 SEQ ID NO:2.

XX

KW Mitochondrial cytochrome b gene; mitochondrial; cytochrome b;

KW identification; criminal investigation; animal poaching; PCR primer; ss.

XX

OS Synthetic.

XX

PN WO200272728-A1.

XX

PD 03-OCT-2002.

XX

PF 28-MAR-2001; 2001WO-IN000055.

XX

PR 28-MAR-2001; 2001WO-IN000055.

XX

PA (COUL) COUNCIL SCI & IND RES.

XX

PI Verma SK, Singh L;

XX

DR WPI; 2003-018945/01.

XX

PT New universal primers, mcb 398 and mcb 869, capable of amplifying a fragment of cytochrome b gene of any animal species, useful for establishing the identity of biological materials and animals for molecular evidence in forensics.

XX

PS Claim 1; Page 116; 128pp; English.

XX

CC The present invention describes universal primers, mcb 398 and mcb 869 (see ABQ83297 and ABQ83298), capable of amplifying a fragment of cytochrome b gene of any animal species in polymerase chain reaction (PCR) and revealing the identity of the biological material of any animal of unknown origin at species and sub-species level. Also described is a method for the identification of the animal from a biological sample. The method is used for animal identification to establish the crime with the criminal beyond a reasonable doubt, to establish the identity of

CC biological materials such as skin, horns confiscated from animal
 CC poachers, if it is that of an endangered species, for the purpose of
 CC molecular evidence of animal hunting and related crime in the court of
 CC law, so that human violation of the wildlife resources could be
 CC controlled, to have an idea of the geographical location of the
 CC commitment of wildlife crime based on the cytochrome b gene haplotype of
 CC poached animal identified by the universal primer invented, to detect the
 CC adulteration of animal meat in food products for the purpose of food
 CC fortification, by the food fortification agencies, to provide a universal
 CC technique for detection of the origin of blood or blood stains collected
 CC from the scene of the crime related to offenses such as murder and rape,
 CC in order to establish the origin of blood found at the scene of the crime
 CC when it sounds as if criminals intentionally spread the blood of an
 CC animal at the scene of the crime to confuse the crime investigators and
 CC forensic scientists with human blood, and so that the method can be
 CC converted to a commercial molecular kit and DNA chips based applications
 CC for wildlife identification in forensics

XX SQ Sequence 25 BP; 9 A; 5 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 8; Length 25;
 Best Local Similarity 100.0%; Pred. No. 0.21; Length 25;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25

DB 1 TACCATGAGGACAAATATCATCTG 25

RESULT 2

ABX49123

ID ABX49123 standard; cDNA; 329 BP.

XX AC ABX49123;

XX DT 21-FEB-2003 (first entry)

XX DE Bovine EST associated with lactation/muscle/fat deposition #14288.

XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
 KW muscle deposition; fat deposition; genome mapping; gene identification;
 KW gene analysis; cattle breeding.

XX OS Bos Taurus.

XX PN US2002137139-A1.

XX PD 26-SEP-2002.

XX PF 24-SEP-2001; 2001US-00960352.

XX PR 12-JAN-1999; 99US-0115707P.

XX PR 11-JAN-2000; 2000US-00480902.

XX PA (BYAT/) BYATT J C.

XX PA (MATH/) MATHIALAGAN N.

XX PA (TAON/) TAO N.

XX PA (WARR/) WARREN W C.

XX PI Byatt JC, Mathialagan N, Tao N, Warren WC;

XX DR WPI; 2003-110599/10.

XX PT New nucleic acid associated with lactation, and muscle and fat
 PT deposition, useful for genome mapping, gene identification and analysis,
 PT cattle breeding, or for genetically improving cattle.

XX PS Claim 2; SEQ ID NO 14288; 245pp; English.

XX CC The invention relates to a purified nucleic acid molecule associated with
 CC lactation or muscle and fat deposition (designated LMFD), derived from
 CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
 CC nucleic acid molecule comprising any of 15112 nucleotide sequences,

CC appearing as ABX34836-ABX49947, or complements of them. Also included are
 CC : (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
 CC acid linked to a promoter and a 3' non-translated sequence that
 CC functions in the cell to cause termination of transcription and addition
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
 CC (2) determining a level or pattern of a molecule in a bovine cell or
 CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
 CC of the 15112 nucleic acid sequences or its complement or fragment) with a
 CC complementary nucleic acid molecule obtained from the bovine cell or
 CC tissue, where hybridisation between the marker nucleic acid and the
 CC complementary nucleic acid permits the detection of the molecule; and (b)
 CC detecting the level or pattern of the complementary nucleic acid, where
 CC the detection of the complementary nucleic acid is predictive of the
 CC level or pattern of the molecule. The LMFD nucleic acid is used for
 CC determining a level or pattern of a molecule in a bovine cell or tissue.
 CC It is useful for genome mapping, gene identification and analysis, cattle
 CC breeding, preparation of constructs for use in cattle gene expression, or
 CC for genetically improving cattle. The present sequence is one of the
 CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
 CC present sequence was not shown in the specification but was obtained in
 CC electronic format from the USPTO web site:

CC seqdata.uspto.gov/sequence.html?DocID=20020137139

XX SQ Sequence 329 BP; 96 A; 78 C; 66 G; 89 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 8; Length 329;

Best Local Similarity 100.0%; Pred. No. 0.26; Length 329;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25

DB 305 TACCATGAGGACAAATATCATCTG 329

RESULT 3

ABX41392

ID ABX41392 standard; cDNA; 346 BP.

XX AC ABX41392;

XX DT 20-FEB-2003 (first entry)

XX DE Bovine EST associated with lactation/muscle/fat deposition #6557.

XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
 KW muscle deposition; fat deposition; genome mapping; gene identification;
 KW gene analysis; cattle breeding.

XX OS Bos Taurus.

XX PN US2002137139-A1.

XX PD 26-SEP-2002.

XX PF 24-SEP-2001; 2001US-00960352.

XX PR 12-JAN-1999; 99US-0115707P.

XX PR 11-JAN-2000; 2000US-00480902.

XX PA (BYAT/) BYATT J C.

XX PA (MATH/) MATHIALAGAN N.

XX PA (TAON/) TAO N.

XX PA (WARR/) WARREN W C.

XX PI Byatt JC, Mathialagan N, Tao N, Warren WC;

XX DR WPI; 2003-110599/10.

XX PT New nucleic acid associated with lactation, and muscle and fat
 PT deposition, useful for genome mapping, gene identification and analysis,
 PT cattle breeding, or for genetically improving cattle.

XX PS Claim 2; SEQ ID NO 6557; 245pp; English.

XX The invention relates to a purified nucleic acid molecule associated with
 CC lactation or muscle and fat deposition (designated LMFD), derived from
 CC cattle, and the LMFD nucleic acid can specifically hybridize to a second
 CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
 CC appearing as ABX34836-ABX49947, or complements of them. Also included are
 CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
 CC acid linked to a promoter and a 3' non- translated sequence that
 CC functions in the cell to cause termination of transcription and addition
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
 CC (2) determining a level or pattern of a molecule in a bovine cell or
 CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
 CC of the 15112 nucleic acid sequences or its complement or fragment) with a
 CC complementary nucleic acid molecule obtained from the bovine cell or
 CC tissue, where hybridisation between the marker nucleic acid and the
 CC complementary nucleic acid permits the detection of the molecule; and (b)
 CC detecting the level or pattern of the complementary nucleic acid, where
 CC the detection of the complementary nucleic acid is predictive of the
 CC level or pattern of the molecule. The LMFD nucleic acid is used for
 CC determining a level or pattern of a molecule in a bovine cell or tissue.
 CC It is useful for genome mapping, gene identification and analysis, cattle
 CC breeding, preparation of constructs for use in cattle gene expression, or
 CC for genetically improving cattle. The present sequence is one of the
 CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
 CC present sequence was not shown in the specification but was obtained in
 CC electronic format from the USPTO web site:
 CC seqdata.uspto.gov/sequence.html?docID=20020137139

XX Sequence 346 BP; 106 A; 82 C; 55 G; 103 T; 0 U; 0 Other;
 Query Match 100.0%; Score 25; DB 8; Length 346;
 Best Local Similarity 100.0%; Pred. No. 0.27;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACATGAGGACAAATATCATCTG 25
 |||||
 Db 174 TACATGAGGACAAATATCATCTG 198

RESULT 4
 ABX41185
 ID ABX41185 standard; cDNA; 353 BP.
 XX
 AC ABX41185;
 XX
 XX
 DT 20-FEB-2003 (first entry)
 XX
 DE Bovine EST associated with lactation/muscle/fat deposition #6350.
 XX
 KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
 KW muscle deposition; fat deposition; genome mapping; gene identification;
 KW gene analysis; cattle breeding.
 XX
 OS Bos Taurus.

XX US2002137139-A1.
 XX
 XX 26-SEP-2002.
 XX
 XX 24-SEP-2001; 2001US-00960352.
 XX
 XX 12-JAN-1999; 99US-0115707P.
 XX 11-JAN-2000; 2000US-00480902.
 XX
 XX (BYAT/) BYATT J C.
 XX (MATH/) MATHIALAGAN N.
 XX (TAON/) TAO N.
 XX (WARR/) WARREN W C.
 XX
 XX Byatt JC, Mathialagan N, Tao N, Warren WC;
 XX WPI; 2003-110599/10.
 XX

PT New nucleic acid associated with lactation, and muscle and fat
 PT deposition, useful for genome mapping, gene identification and analysis,
 PT cattle breeding, or for genetically improving cattle.
 XX

XX Claim 2; SEQ ID NO 6350; 245pp; English.

XX The invention relates to a purified nucleic acid molecule associated with
 CC lactation or muscle and fat deposition (designated LMFD), derived from
 CC cattle, and the LMFD nucleic acid can specifically hybridize to a second
 CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
 CC appearing as ABX34836-ABX49947, or complements of them. Also included are
 CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
 CC acid linked to a promoter and a 3' non- translated sequence that
 CC functions in the cell to cause termination of transcription and addition
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
 CC (2) determining a level or pattern of a molecule in a bovine cell or
 CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
 CC of the 15112 nucleic acid sequences or its complement or fragment) with a
 CC complementary nucleic acid molecule obtained from the bovine cell or
 CC tissue, where hybridisation between the marker nucleic acid and the
 CC complementary nucleic acid permits the detection of the molecule; and (b)
 CC detecting the level or pattern of the complementary nucleic acid, where
 CC the detection of the complementary nucleic acid is predictive of the
 CC level or pattern of the molecule. The LMFD nucleic acid is used for
 CC determining a level or pattern of a molecule in a bovine cell or tissue.
 CC It is useful for genome mapping, gene identification and analysis, cattle
 CC breeding, preparation of constructs for use in cattle gene expression, or
 CC for genetically improving cattle. The present sequence is one of the
 CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
 CC present sequence was not shown in the specification but was obtained in
 CC electronic format from the USPTO web site:
 CC seqdata.uspto.gov/sequence.html?docID=20020137139

XX Sequence 353 BP; 106 A; 91 C; 56 G; 100 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 8; Length 353;
 Best Local Similarity 100.0%; Pred. No. 0.27;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACATGAGGACAAATATCATCTG 25
 |||||
 Db 324 TACATGAGGACAAATATCATCTG 348

RESULT 5
 ABX42082
 ID ABX42082 standard; cDNA; 380 BP.
 XX
 AC ABX42082;

XX 20-FEB-2003 (first entry)

XX Bovine EST associated with lactation/muscle/fat deposition #7247.

XX Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
 KW muscle deposition; fat deposition; genome mapping; gene identification;
 KW gene analysis; cattle breeding.

XX Bos Taurus.

XX US2002137139-A1.

XX 26-SEP-2002.

XX 24-SEP-2001; 2001US-00960352.

XX 12-JAN-1999; 99US-0115707P.

XX 11-JAN-2000; 2000US-00480902.

XX (BYAT/) BYATT J C.

XX (MATH/) MATHIALAGAN N.

XX (TAON/) TAO N.

XX (WARR/) WARREN W C.

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XX PI Byatt JC, Mathialagan N, Tao N, Warren WC;
XX DR WPI; 2003-110599/10.
XX PT New nucleic acid associated with lactation, and muscle and fat
XX PT deposition, useful for genome mapping, gene identification and analysis,
XX PT cattle breeding, or for genetically improving cattle.
XX PS Claim 2; SEQ ID NO 7247; 245pp; English.
XX CC The invention relates to a purified nucleic acid molecule associated with
XX CC lactation or muscle and fat deposition (designated LMFD), derived from
XX CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
XX CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
XX CC appearing as ABX34836-ABX49947, or complements of them. Also included are
XX CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
XX CC acid linked to a promoter and a 3' non- translated sequence that
XX CC functions in the cell to cause termination of transcription and addition
XX CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
XX CC (2) determining a level or pattern of a molecule in a bovine cell or
XX CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
XX CC of the 15112 nucleic acid sequences or its complement or fragment) with a
XX CC complementary nucleic acid molecule obtained from the bovine cell or
XX CC tissue, where hybridisation between the marker nucleic acid and the
XX CC complementary nucleic acid permits the detection of the molecule; and (b)
XX CC determining a level or pattern of a molecule in a bovine cell or tissue.
XX CC It is useful for genome mapping, gene identification and analysis, cattle
XX CC breeding, preparation of constructs for use in cattle gene expression, or
XX CC for genetically improving cattle. The present sequence is one of the
XX CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
XX CC present sequence was not shown in the specification but was obtained in
XX CC electronic format from the USPTO web site:
XX CC seqdata.uspto.gov/sequence.html?DocID=20020137139
XX SQ Sequence 380 BP; 112 A; 96 C; 61 G; 111 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 8; Length 380;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
Db 174 TACCATGAGGACAAATATCATCTG 198

RESULT 6
ABX36231
ID ABX36231 standard; cDNA; 388 BP.
AC ABX36231;
XX AC
XX DT 20-FEB-2003 (first entry)
XX DE Bovine EST associated with lactation/muscle/fat deposition #1396.
XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
XX KW muscle deposition; fat deposition; genome mapping; gene identification;
XX KW gene analysis; cattle breeding.
XX OS Bos Taurus.
XX PN US2002137139-A1.
XX PD 26-SEP-2002.
XX PF 24-SEP-2001; 2001US-00960352.
XX PR 12-JAN-1999; 99US-0115707P.
XX PR 11-JAN-2000; 2000US-00480902.
XX PR

XX PA (BYATT/) BYATT J C.
XX PA (MATH/) MATHIALAGAN N.
XX PA (TAON/) TAO N.
XX PA (WARR/) WARREN W C.
XX PI Byatt JC, Mathialagan N, Tao N, Warren WC;
XX DR WPI; 2003-110599/10.
XX PT New nucleic acid associated with lactation, and muscle and fat
XX PT deposition, useful for genome mapping, gene identification and analysis,
XX PT cattle breeding, or for genetically improving cattle.
XX PS Claim 2; SEQ ID NO 1396; 245pp; English.
XX CC The invention relates to a purified nucleic acid molecule associated with
XX CC lactation or muscle and fat deposition (designated LMFD), derived from
XX CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
XX CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
XX CC appearing as ABX34836-ABX49947, or complements of them. Also included are
XX CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
XX CC acid linked to a promoter and a 3' non- translated sequence that
XX CC functions in the cell to cause termination of transcription and addition
XX CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
XX CC (2) determining a level or pattern of a molecule in a bovine cell or
XX CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
XX CC of the 15112 nucleic acid sequences or its complement or fragment) with a
XX CC complementary nucleic acid molecule obtained from the bovine cell or
XX CC tissue, where hybridisation between the marker nucleic acid and the
XX CC complementary nucleic acid permits the detection of the molecule; and (b)
XX CC detecting the level or pattern of the complementary nucleic acid, where
XX CC the detection of the complementary nucleic acid is predictive of the
XX CC level or pattern of the molecule. The LMFD nucleic acid is used for
XX CC determining a level or pattern of a molecule in a bovine cell or tissue.
XX CC It is useful for genome mapping, gene identification and analysis, cattle
XX CC breeding, preparation of constructs for use in cattle gene expression, or
XX CC for genetically improving cattle. The present sequence is one of the
XX CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
XX CC present sequence was not shown in the specification but was obtained in
XX CC electronic format from the USPTO web site:
XX CC seqdata.uspto.gov/sequence.html?DocID=20020137139
XX SQ Sequence 388 BP; 118 A; 111 C; 56 G; 101 T; 0 U; 2 Other;

Query Match 100.0%; Score 25; DB 8; Length 388;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
Db 109 TACCATGAGGACAAATATCATCTG 133

RESULT 7
ABX42640
ID ABX42640 standard; cDNA; 397 BP.
XX AC
XX AC ABX42640;
XX DT 20-FEB-2003 (first entry)
XX DE Bovine EST associated with lactation/muscle/fat deposition #7805.
XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
XX KW muscle deposition; fat deposition; genome mapping; gene identification;
XX KW gene analysis; cattle breeding.
XX OS Bos Taurus.
XX PN US2002137139-A1.
XX PD 26-SEP-2002.
XX PR

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XX PF 24-SEP-2001; 2001US-00960352.
 XX XX 12-JAN-1999; 99US-0115707P.
 XX PR 11-JAN-2000; 2000US-00480902.
 XX XX (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARE/) WARREN W C.
 XX XX Byatt JC, Mathialagan N, Tao N, Warren WC;
 XX XX WPI; 2003-110599/10.
 XX XX New nucleic acid associated with lactation, and muscle and fat
 PT deposition, useful for genome mapping, gene identification and analysis,
 PT cattle breeding, or for genetically improving cattle.
 XX XX Claim 2; SEQ ID NO 7805; 245pp; English.
 XX XX The invention relates to a purified nucleic acid molecule associated with
 CC lactation or muscle and fat deposition (designated LMFD), derived from
 CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
 CC nucleic acid molecule comprising any of 1512 nucleotide sequences,
 CC appearing as ABX34836-ABX49947, or complements of them. Also included are
 CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
 CC acid linked to a promoter and a 3' non- translated sequence that
 CC functions in the cell to cause termination of transcription and addition
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
 CC (2) determining a level or pattern of a molecule in a bovine cell or
 CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
 CC of the 1512 nucleic acid sequences or its complement or fragment) with a
 CC the detection of the complementary nucleic acid is predictive of the
 CC level or pattern of the molecule. The LMFD nucleic acid is used for
 CC determining a level or pattern of a molecule in a bovine cell or tissue.
 CC It is useful for genome mapping, gene identification and analysis, cattle
 CC breeding, preparation of constructs for use in cattle gene expression, or
 CC for genetically improving cattle. The present sequence is one of the
 CC 1512 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
 CC present sequence was not shown in the specification but was obtained in
 CC electronic format from the USPTO web site:
 CC seqdata.uspto.gov/sequence.html?DocID=20020137139
 XX XX Sequence 397 BP; 122 A; 109 C; 58 G; 108 T; 0 U; 0 Other;
 Query Match 100.0%; Score 25; DB 8; Length 397;
 Best Local Similarity 100.0%; Pred. No. 0.27;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TACCATGAGGACAAATATCATCTG 25
 Db 125 TACCATGAGGACAAATATCATCTG 149
 RESULT 8
 ABX47053
 ID ABX47053 standard; cDNA; 402 BP.
 XX AC ABX47053;
 XX XX 21-FEB-2003 (first entry)
 XX XX Bovine EST associated with lactation/muscle/fat deposition #12218.
 XX XX Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
 KW muscle deposition; fat deposition; genome mapping; gene identification;
 KW gene analysis; cattle breeding.

OS Bos Taurus.
 XX US2002137139-A1.
 XX 26-SEP-2002.
 XX 24-SEP-2001; 2001US-00960352.
 XX 12-JAN-1999; 99US-0115707P.
 PR 11-JAN-2000; 2000US-00480902.
 XX (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARE/) WARREN W C.
 XX XX Byatt JC, Mathialagan N, Tao N, Warren WC;
 XX XX WPI; 2003-110599/10.
 XX XX New nucleic acid associated with lactation, and muscle and fat
 PT deposition, useful for genome mapping, gene identification and analysis,
 PT cattle breeding, or for genetically improving cattle.
 XX XX Claim 2; SEQ ID NO 12218; 245pp; English.
 XX XX The invention relates to a purified nucleic acid molecule associated with
 CC lactation or muscle and fat deposition (designated LMFD), derived from
 CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
 CC nucleic acid molecule comprising any of 1512 nucleotide sequences,
 CC appearing as ABX34836-ABX49947, or complements of them. Also included are
 CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
 CC acid linked to a promoter and a 3' non- translated sequence that
 CC functions in the cell to cause termination of transcription and addition
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
 CC (2) determining a level or pattern of a molecule in a bovine cell or
 CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
 CC of the 1512 nucleic acid sequences or its complement or fragment) with a
 CC the detection of the complementary nucleic acid is predictive of the
 CC level or pattern of the molecule. The LMFD nucleic acid is used for
 CC determining a level or pattern of a molecule in a bovine cell or tissue.
 CC It is useful for genome mapping, gene identification and analysis, cattle
 CC breeding, preparation of constructs for use in cattle gene expression, or
 CC for genetically improving cattle. The present sequence is one of the
 CC 1512 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
 CC present sequence was not shown in the specification but was obtained in
 CC electronic format from the USPTO web site:
 CC seqdata.uspto.gov/sequence.html?DocID=20020137139
 XX XX Sequence 402 BP; 125 A; 107 C; 62 G; 108 T; 0 U; 0 Other;
 Query Match 100.0%; Score 25; DB 8; Length 402;
 Best Local Similarity 100.0%; Pred. No. 0.27;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TACCATGAGGACAAATATCATCTG 25
 Db 309 TACCATGAGGACAAATATCATCTG 333
 RESULT 9
 ABX44209
 ID ABX44209 standard; cDNA; 409 BP.
 XX AC ABX44209;
 XX XX 21-FEB-2003 (first entry)
 XX XX Bovine EST associated with lactation/muscle/fat deposition #9374.

XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
 KW muscle deposition; fat deposition; genome mapping; gene identification;
 KW gene analysis; cattle breeding.
 OS Bos Taurus.
 XX US2002137139-A1.
 PD 26-SEP-2002.
 XX 24-SEP-2001; 2001US-00960352.
 XX 12-JAN-1999; 99US-0115707P.
 PR 11-JAN-2000; 2000US-00480902.
 XX (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 XX Byatt JC, Mathialagan N, Tao N, Warren WC;
 XX WPI; 2003-110599/10.
 XX New nucleic acid associated with lactation, and muscle and fat
 PT deposition, useful for genome mapping, gene identification and analysis,
 PT cattle breeding, or for genetically improving cattle.
 XX Claim 2; SEQ ID NO 9374; 245pp; English.
 XX The invention relates to a purified nucleic acid molecule associated with
 CC lactation or muscle and fat deposition (designated LMFD), derived from
 CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
 CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
 CC appearing as ABX34836-ABX49947, or complements of them. Also included are
 CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
 CC acid linked to a promoter and a 3' non- translated sequence that
 CC functions in the cell to cause termination of transcription and addition
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
 CC (2) determining a level or pattern of a molecule in a bovine cell or
 CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
 CC of the 15112 nucleic acid sequences or its complement or fragment) with a
 CC complementary nucleic acid molecule obtained from the bovine cell or
 CC tissue, where hybridisation between the marker nucleic acid and the
 CC complementary nucleic acid permits the detection of the molecule; and (b)
 CC detecting the level or pattern of the complementary nucleic acid, where
 CC the detection of the complementary nucleic acid is predictive of the
 CC level or pattern of a molecule in a bovine cell or tissue.
 CC It is useful for genome mapping, gene identification and analysis, cattle
 CC breeding, preparation of constructs for use in cattle gene expression, or
 CC for genetically improving cattle. The present sequence is one of the
 CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
 CC present sequence was not shown in the specification but was obtained in
 CC electronic format from the USPTO web site:
 CC seqdata.uspto.gov/sequence.html?docID=20020137139
 XX SQ Sequence 409 BP; 127 A; 108 C; 62 G; 112 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 8; Length 409;
 Best Local Similarity 100.0%; Pred. No. 0.27;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
 DB 379 TACCATGAGGACAAATATCATCTG 403

RESULT 10
 ABX42249
 ID ABX42249 standard; cDNA; 409 BP.
 XX

AC ABX42249;
 XX 20-FEB-2003 (first entry)
 DT Bovine EST associated with lactation/muscle/fat deposition #7414.
 XX Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
 KW muscle deposition; fat deposition; genome mapping; gene identification;
 KW gene analysis; cattle breeding.
 XX Bos Taurus.
 XX US2002137139-A1.
 PD 26-SEP-2002.
 XX 24-SEP-2001; 2001US-00960352.
 XX 12-JAN-1999; 99US-0115707P.
 PR 11-JAN-2000; 2000US-00480902.
 XX (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 XX Byatt JC, Mathialagan N, Tao N, Warren WC;
 XX WPI; 2003-110599/10.
 XX New nucleic acid associated with lactation, and muscle and fat
 PT deposition, useful for genome mapping, gene identification and analysis,
 PT cattle breeding, or for genetically improving cattle.
 XX Claim 2; SEQ ID NO 7414; 245pp; English.
 XX The invention relates to a purified nucleic acid molecule associated with
 CC lactation or muscle and fat deposition (designated LMFD), derived from
 CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
 CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
 CC appearing as ABX34836-ABX49947, or complements of them. Also included are
 CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
 CC acid linked to a promoter and a 3' non- translated sequence that
 CC functions in the cell to cause termination of transcription and addition
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
 CC (2) determining a level or pattern of a molecule in a bovine cell or
 CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
 CC of the 15112 nucleic acid sequences or its complement or fragment) with a
 CC complementary nucleic acid molecule obtained from the bovine cell or
 CC tissue, where hybridisation between the marker nucleic acid and the
 CC complementary nucleic acid permits the detection of the molecule; and (b)
 CC detecting the level or pattern of the complementary nucleic acid, where
 CC the detection of the complementary nucleic acid is predictive of the
 CC level or pattern of a molecule in a bovine cell or tissue.
 CC It is useful for genome mapping, gene identification and analysis, cattle
 CC breeding, preparation of constructs for use in cattle gene expression, or
 CC for genetically improving cattle. The present sequence is one of the
 CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
 CC present sequence was not shown in the specification but was obtained in
 CC electronic format from the USPTO web site:
 CC seqdata.uspto.gov/sequence.html?docID=20020137139
 XX SQ Sequence 409 BP; 128 A; 106 C; 63 G; 111 T; 0 U; 1 Other;

Query Match 100.0%; Score 25; DB 8; Length 409;
 Best Local Similarity 100.0%; Pred. No. 0.27;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
 DB 373 TACCATGAGGACAAATATCATCTG 397

RESULT 11
ABX39507
ID ABX39507 standard; cDNA; 409 BP.
XX
AC ABX39507;
XX
AC
XX 20-FEB-2003 (first entry)
XX
DE Bovine EST associated with lactation/muscle/fat deposition #4672.
XX
KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
KW muscle deposition; fat deposition; genome mapping; gene identification;
KW gene analysis; cattle breeding.
XX
OS Bos Taurus.
XX
XX US2002137139-A1.
XX
XX 26-SEP-2002.
XX
XX 24-SEP-2001; 2001US-00960352.
XX
XX 12-JAN-1999; 99US-0115707P.
XX
XX 11-JAN-2000; 2000US-00480902.
XX
XX (BYAT/) BYATT J C.
XX (MATH/) MATHIALAGAN N.
XX (TAON/) TAO N.
XX (WARR/) WARREN W C.
XX
XX Byatt JC, Mathialagan N, Tao N, Warren WC;
XX WPI; 2003-110599/10.
XX
XX New nucleic acid associated with lactation, and muscle and fat
XX deposition, useful for genome mapping, gene identification and analysis,
XX cattle breeding, or for genetically improving cattle.
XX
XX Claim 2; SEQ ID NO 4672; 245pp; English.
XX
XX The invention relates to a purified nucleic acid molecule associated with
XX lactation or muscle and fat deposition (designated LMFD), derived from
XX cattle, and the LMFD nucleic acid can specifically hybridise to a second
XX nucleic acid molecule comprising any of 15112 nucleotide sequences,
XX appearing as ABX34836-ABX49947, or complements of them. Also included are
XX ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
XX acid linked to a promoter and a 3' non- translated sequence that
XX functions in the cell to cause termination of transcription and addition
XX of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
XX (2) determining a level or pattern of a molecule in a bovine cell or
XX tissue comprising: (a) incubating a marker nucleic acid (comprising any
XX of the 15112 nucleic acid sequences or its complement or fragment) with a
XX complementary nucleic acid molecule obtained from the bovine cell or
XX tissue, where hybridisation between the marker nucleic acid and the
XX complementary nucleic acid permits the detection of the molecule; and (b)
XX detecting the level or pattern of the complementary nucleic acid, where
XX the detection of the complementary nucleic acid is predictive of the
XX level or pattern of the molecule. The LMFD nucleic acid is used for
XX determining a level or pattern of a molecule in a bovine cell or tissue.
XX It is useful for genome mapping, gene identification and analysis, cattle
XX breeding, preparation of constructs for use in cattle gene expression, or
XX for genetically improving cattle. The present sequence is one of the
XX 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
XX present sequence was not shown in the USPTO web site:
XX seqdata.uspto.gov/sequence.html?DocID=20020137139
XX
SQ Sequence 409 BP; 125 A; 112 C; 61 G; 111 T; 0 U; 0 Other;
Query Match 100.0%; Score 25; DB 8; Length 409;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
|||||
Db 340 TACCATGAGGACAAATATCATCTG 364
|||
RESULT 12
ABX43333
ID ABX43333 standard; cDNA; 411 BP.
XX
AC ABX43333;
XX
XX 20-FEB-2003 (first entry)
XX
XX Bovine EST associated with lactation/muscle/fat deposition #8498.
XX
XX Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
KW muscle deposition; fat deposition; genome mapping; gene identification;
KW gene analysis; cattle breeding.
XX
OS Bos Taurus.
XX
XX US2002137139-A1.
XX
XX 26-SEP-2002.
XX
XX 24-SEP-2001; 2001US-00960352.
XX
XX 12-JAN-1999; 99US-0115707P.
XX
XX 11-JAN-2000; 2000US-00480902.
XX
XX (BYAT/) BYATT J C.
XX (MATH/) MATHIALAGAN N.
XX (TAON/) TAO N.
XX (WARR/) WARREN W C.
XX
XX Byatt JC, Mathialagan N, Tao N, Warren WC;
XX WPI; 2003-110599/10.
XX
XX New nucleic acid associated with lactation, and muscle and fat
XX deposition, useful for genome mapping, gene identification and analysis,
XX cattle breeding, or for genetically improving cattle.
XX
XX Claim 2; SEQ ID NO 8498; 245pp; English.
XX
XX The invention relates to a purified nucleic acid molecule associated with
XX lactation or muscle and fat deposition (designated LMFD), derived from
XX cattle, and the LMFD nucleic acid can specifically hybridise to a second
XX nucleic acid molecule comprising any of 15112 nucleotide sequences,
XX appearing as ABX34836-ABX49947, or complements of them. Also included are
XX ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
XX acid linked to a promoter and a 3' non- translated sequence that
XX functions in the cell to cause termination of transcription and addition
XX of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
XX (2) determining a level or pattern of a molecule in a bovine cell or
XX tissue comprising: (a) incubating a marker nucleic acid (comprising any
XX of the 15112 nucleic acid sequences or its complement or fragment) with a
XX complementary nucleic acid molecule obtained from the bovine cell or
XX tissue, where hybridisation between the marker nucleic acid and the
XX complementary nucleic acid permits the detection of the molecule; and (b)
XX detecting the level or pattern of the complementary nucleic acid, where
XX the detection of the complementary nucleic acid is predictive of the
XX level or pattern of the molecule. The LMFD nucleic acid is used for
XX determining a level or pattern of a molecule in a bovine cell or tissue.
XX It is useful for genome mapping, gene identification and analysis, cattle
XX breeding, preparation of constructs for use in cattle gene expression, or
XX for genetically improving cattle. The present sequence is one of the
XX 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
XX present sequence was not shown in the USPTO web site:
XX seqdata.uspto.gov/sequence.html?DocID=20020137139
XX

SQ Sequence 411 BP; 130 A; 109 C; 61 G; 111 T; 0 U; 0 Other;
 Query Match 100.0%; Score 25; DB 8; Length 411;
 Best Local Similarity 100.0%; Pred. No. 0.27; 0; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TACCATGAGGACAAATATCATCTG 25
 |||||
 DB 378 TACCATGAGGACAAATATCATCTG 402
 |||||
 RESULT 13
 ABX35955
 ID ABX35955 standard; cDNA; 412 BP.
 XX AC ABX35955;
 XX DT 20-FEB-2003 (first entry)
 XX DE Bovine EST associated with lactation/muscle/fat deposition #1120.
 XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
 KW muscle deposition; fat deposition; genome mapping; gene identification;
 KW gene analysis; cattle breeding.
 XX OS Bos Taurus.
 XX US2002137139-A1.
 XX PN 12-JAN-1999; 99US-0115707P.
 XX PR 11-JAN-2000; 2000US-00480902.
 XX PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 XX PI Byatt JC, Mathialagan N, Tao N, Warren WC;
 DR WPI; 2003-110599/10.
 PS New nucleic acid associated with lactation, and muscle and fat
 PT deposition, useful for genome mapping, gene identification and analysis,
 PT cattle breeding, or for genetically improving cattle.
 XX Claim 2; SEQ ID NO 1120; 245pp; English.
 CC The invention relates to a purified nucleic acid molecule associated with
 CC lactation or muscle and fat deposition (designated LMFD), derived from
 CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
 CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
 CC appearing as ABX34836-ABX49947, or complements of them. Also included are
 CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
 CC acid linked to a promoter and a 3' non- translated sequence that
 CC functions in the cell to cause termination of transcription and addition
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
 CC (2) determining a level or pattern of a molecule in a bovine cell or
 CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
 CC of the 15112 nucleic acid sequences or its complement or fragment) with a
 CC complementary nucleic acid molecule obtained from the bovine cell or
 CC tissue, where hybridisation between the marker nucleic acid and the
 CC complementary nucleic acid permits the detection of the molecule; and
 CC detecting the level or pattern of the complementary nucleic acid, where
 CC It is useful for genome mapping, gene identification and analysis, cattle
 CC breeding, preparation of constructs for use in cattle gene expression, or
 CC for genetically improving cattle. The present sequence is one of the

CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
 CC present sequence was not shown in the specification but was obtained in
 CC electronic format from the USPTO web site:
 CC seqdata.uspto.gov/sequence.html?DocID=20020137139
 XX SQ Sequence 412 BP; 118 A; 108 C; 61 G; 125 T; 0 U; 0 Other;
 Query Match 100.0%; Score 25; DB 8; Length 412;
 Best Local Similarity 100.0%; Pred. No. 0.27; 0; Indels 0; Gaps 0;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TACCATGAGGACAAATATCATCTG 25
 |||||
 DB 372 TACCATGAGGACAAATATCATCTG 396
 |||||
 RESULT 14
 ABX37092
 ID ABX37092 standard; cDNA; 413 BP.
 XX AC ABX37092;
 XX DT 20-FEB-2003 (first entry)
 XX DE Bovine EST associated with lactation/muscle/fat deposition #2257.
 XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
 KW muscle deposition; fat deposition; genome mapping; gene identification;
 KW gene analysis; cattle breeding.
 XX OS Bos Taurus.
 XX US2002137139-A1.
 XX PN 26-SEP-2002.
 XX PD 24-SEP-2001; 2001US-00960352.
 XX PF 12-JAN-1999; 99US-0115707P.
 XX PR 11-JAN-2000; 2000US-00480902.
 XX PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 XX PI Byatt JC, Mathialagan N, Tao N, Warren WC;
 DR WPI; 2003-110599/10.
 PS New nucleic acid associated with lactation, and muscle and fat
 PT deposition, useful for genome mapping, gene identification and analysis,
 PT cattle breeding, or for genetically improving cattle.
 XX Claim 2; SEQ ID NO 2257; 245pp; English.
 CC The invention relates to a purified nucleic acid molecule associated with
 CC lactation or muscle and fat deposition (designated LMFD), derived from
 CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
 CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
 CC appearing as ABX34836-ABX49947, or complements of them. Also included are
 CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
 CC acid linked to a promoter and a 3' non- translated sequence that
 CC functions in the cell to cause termination of transcription and addition
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
 CC (2) determining a level or pattern of a molecule in a bovine cell or
 CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
 CC of the 15112 nucleic acid sequences or its complement or fragment) with a
 CC complementary nucleic acid molecule obtained from the bovine cell or
 CC tissue, where hybridisation between the marker nucleic acid and the
 CC complementary nucleic acid permits the detection of the molecule; and (b)
 CC detecting the level or pattern of the complementary nucleic acid, where
 CC the detection of the complementary nucleic acid is predictive of the

CC level or pattern of the molecule. The LMFD nucleic acid is used for
 CC determining a level or pattern of a molecule in a bovine cell or tissue.
 CC It is useful for genome mapping, gene identification and analysis, cattle
 CC breeding, preparation of constructs for use in cattle gene expression, or
 CC for genetically improving cattle. The present sequence is one of the
 CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
 CC present sequence was not shown in the specification but was obtained in
 CC electronic format from the USPTO web site:
 CC seqdata.uspto.gov/sequence.html?DocID=20020137139

XX Sequence 413 BP; 130 A; 109 C; 62 G; 112 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 8; Length 413;
 Best Local Similarity 100.0%; Pred. No. 0.27;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
 |||||
 Db 384 TACCATGAGGACAAATATCATCTG 408

RESULT 15

ABX46099
 ID ABX46099 standard; cDNA; 414 BP.

XX AC ABX46099;

XX DT 21-FEB-2003 (first entry)

XX DE Bovine EST associated with lactation/muscle/fat deposition #11264.

XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;

XX KW muscle deposition; fat deposition; genome mapping; gene identification;

XX KW gene analysis; cattle breeding.

XX OS Bos Taurus.

XX PN US2002137139-A1.

XX PD 26-SEP-2002.

XX PF 24-SEP-2001; 2001US-00960352.

XX PR 12-JAN-1999; 99US-0115707P.

XX PR 11-JAN-2000; 2000US-00480302.

XX PA (BYAT/) BYATT J C.

XX PA (MATH/) MATHIALAGAN N.

XX PA (TAON/) TAO N.

XX PA (WARR/) WARREN W C.

XX PI Byatt JC, Mathialagan N, Tao N, Warren WC;

XX DR WPI; 2003-110599/10.

XX PT New nucleic acid associated with lactation, and muscle and fat
 PT deposition, useful for genome mapping, gene identification and analysis,
 PT cattle breeding, or for genetically improving cattle.

XX PS Claim 2; SEQ ID NO 11264; 245pp; English.

XX The invention relates to a purified nucleic acid molecule associated with
 CC lactation or muscle and fat deposition (designated LMFD), derived from
 CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
 CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
 CC appearing as ABX34836-ABX49947, or complements of them. Also included are
 CC : (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
 CC acid linked to a promoter and a 3' non- translated sequence that
 CC functions in the cell to cause termination of transcription and addition
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
 CC (2) determining a level or pattern of a molecule in a bovine cell or
 CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
 CC of the 15112 nucleic acid sequences or its complement or fragment) with a

CC complementary nucleic acid molecule obtained from the bovine cell or
 CC tissue, where hybridisation between the marker nucleic acid and the
 CC complementary nucleic acid permits the detection of the molecule; and (b)
 CC detecting the level or pattern of the complementary nucleic acid, where
 CC the detection of the complementary nucleic acid is predictive of the
 CC level or pattern of the molecule. The LMFD nucleic acid is used for
 CC determining a level or pattern of a molecule in a bovine cell or tissue.
 CC It is useful for genome mapping, gene identification and analysis, cattle
 CC breeding, preparation of constructs for use in cattle gene expression, or
 CC for genetically improving cattle. The present sequence is one of the
 CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
 CC present sequence was not shown in the specification but was obtained in
 CC electronic format from the USPTO web site:
 CC seqdata.uspto.gov/sequence.html?DocID=20020137139

XX Sequence 414 BP; 130 A; 110 C; 61 G; 113 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 8; Length 414;

Best Local Similarity 100.0%; Pred. No. 0.27;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25

|||||

Db 384 TACCATGAGGACAAATATCATCTG 408

Search completed: November 17, 2004, 00:09:08

Job time : 43.7744 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 23:55:00 ; Search time 8.89101 Seconds
(without alignments)
1998.616 Million cell updates/sec

Title: US-09-821-782E-1

Perfect score: 25

Sequence: 1 taccatgagacaaatattcattctg 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PTCUS COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21.8	87.2	759	4	US-09-270-767-11513
2	20.2	80.8	255	4	US-09-702-705-719
3	20.2	80.8	255	4	US-09-736-457-719
4	20.2	80.8	255	4	US-09-614-124B-719
5	20.2	80.8	255	4	US-09-671-325-719
6	20.2	80.8	255	4	US-09-589-184-719
7	20.2	80.8	255	4	US-09-658-824-719
8	20.2	80.8	1140	4	US-09-377-497-7
9	20.2	80.8	16568	4	US-09-525-906-1
10	20.2	80.8	16569	3	US-09-889-889-2
11	20.2	80.8	16569	3	US-09-377-856-1
12	20.2	80.8	16569	4	US-09-302-681-2
13	20.2	80.8	16569	4	US-09-098-079-2
14	20.2	80.8	16569	4	US-10-053-611-1
15	20	80.0	34	1	US-07-825-959-8
16	20	80.0	34	1	US-08-131-324-8
17	20	80.0	34	1	US-08-647-584-6
18	20	80.0	34	3	US-09-358-972-255
19	20	80.0	34	3	US-09-406-064-48
20	20	80.0	34	3	US-09-383-316-95
21	20	80.0	34	4	US-07-788-847-48
22	20	80.0	34	4	US-09-790-417-255
23	18.4	73.6	20	1	US-08-647-584-9
24	18.4	73.6	20	1	US-08-647-584-11
25	18.2	72.8	3176	2	US-08-910-733-17
26	18.2	72.8	3176	2	US-08-910-884-17
27	17.8	71.2	1624	1	US-08-255-670A-1

28	17.6	70.4	26	1	US-07-971-160-35	Sequence 35, Appl
29	17.6	70.4	26	1	US-08-336-241-35	Sequence 35, Appl
30	17.6	70.4	26	2	US-08-465-273-35	Sequence 35, Appl
31	17.6	70.4	26	2	US-09-119-024-35	Sequence 35, Appl
32	17.6	70.4	26	2	US-08-417-226-35	Sequence 35, Appl
33	17.6	70.4	26	3	US-09-196-131-35	Sequence 35, Appl
34	17.6	70.4	26	3	US-08-643-732-35	Sequence 35, Appl
35	17.6	70.4	26	4	US-09-836-169-35	Sequence 4131, Ap
36	17	68.0	286	4	US-09-313-294A-4131	Sequence 4383, Ap
37	17	68.0	232	4	US-09-313-294A-4383	Sequence 27053, A
38	17	68.0	1637	4	US-09-270-767-27053	Sequence 1666, A
39	17	68.0	3264	4	US-09-270-767-11466	Sequence 11466, A
40	17	68.0	16950	3	US-09-453-702B-166	Sequence 1, Appl
41	17	68.0	1230025	4	US-09-198-452A-1	Sequence 29, Appl
42	16.8	67.2	1067	4	US-09-369-247-29	Sequence 26, Appl
43	16.6	66.4	224	2	US-08-569-166-26	Sequence 2273, Ap
44	16.6	66.4	717	4	US-09-489-039A-2273	Sequence 6, Appl
45	16.6	66.4	1434	4	US-09-700-397-6	

ALIGNMENTS

RESULT 1

US-09-270-767-11513
; Sequence 11513, Application US/09270767
; Patent No. 6703491

; GENERAL INFORMATION:

; APPLICANT: Homburger et al.

; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

; FILE REFERENCE: File Reference: 7326-094

; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17

; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 11513

; LENGTH: 759

; TYPE: DNA

; ORGANISM: Drosophila melanogaster

US-09-270-767-11513

Query Match 87.2%; Score 21.8; DB 4; Length 759;

Best Local Similarity 92.0%; Pred. No. 0.52;

Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TACCATGAGGACAAATATCATTCG 25

Db 656 TACCTTGAGGACAAATATCATTTG 680

RESULT 2

US-09-702-705-719

; Sequence 719, Application US/09702705

; Patent No. 6504010

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Lodes, Michael A.

; APPLICANT: Fanger, Gary

; APPLICANT: Vedvick, Tom

; APPLICANT: Carter, Darrick

; APPLICANT: Retter, Marc

; APPLICANT: Mannion, Jane

; APPLICANT: Fan, Liqun

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.478C14

; CURRENT APPLICATION NUMBER: US/09/702,705

; CURRENT FILING DATE: 2000-10-30

; NUMBER OF SEQ ID NOS: 1833

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 719

; LENGTH: 255

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; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(255)
; OTHER INFORMATION: n = A,T,C or G
US-09-702-705-719

Query Match      80.8%; Score 20.2; DB 4; Length 255;
Best Local Similarity 88.0%; Pred. No. 2.4;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
   |||||
Db 96 TCCCGTGAGGCCAAATATCATCTG 120

RESULT 3
US-09-736-457-719
; Sequence 719, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedwick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 719
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(255)
; OTHER INFORMATION: n = A,T,C or G
US-09-736-457-719

Query Match      80.8%; Score 20.2; DB 4; Length 255;
Best Local Similarity 88.0%; Pred. No. 2.4;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
   |||||
Db 96 TCCCGTGAGGCCAAATATCATCTG 120

RESULT 4
US-09-614-124B-719
; Sequence 719, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedwick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER

; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 719
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(255)
; OTHER INFORMATION: n = A,T,C or G
US-09-614-124B-719

Query Match      80.8%; Score 20.2; DB 4; Length 255;
Best Local Similarity 88.0%; Pred. No. 2.4;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
   |||||
Db 96 TCCCGTGAGGCCAAATATCATCTG 120

RESULT 5
US-09-671-325-719
; Sequence 719, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedwick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 719
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(255)
; OTHER INFORMATION: n = A,T,C or G
US-09-671-325-719

Query Match      80.8%; Score 20.2; DB 4; Length 255;
Best Local Similarity 88.0%; Pred. No. 2.4;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
   |||||
Db 96 TCCCGTGAGGCCAAATATCATCTG 120

RESULT 6
US-09-589-184-719
; Sequence 719, Application US/09589184
; Patent No. 6686447
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
```

; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.47808
; CURRENT APPLICATION NUMBER: US/09/589,184
; CURRENT FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 827
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 719
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(255)
; OTHER INFORMATION: n = A,T,C or G
US-09-589-184-719

Query Match 80.8%; Score 20.2; DB 4; Length 255;
Best Local Similarity 88.0%; Pred. No. 2.4;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TACCATGAGGACAAATATCATCTG 25
Db 96 TCCGTGAGGCCAAATATCATCTG 120

RESULT 7
US-09-658-824-719
; Sequence 719, Application US/09658824
; Patent No. 6746646
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C11
; CURRENT APPLICATION NUMBER: US/09/658,824
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 1788
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 719
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(255)
; OTHER INFORMATION: n = A,T,C or G
US-09-658-824-719

Query Match 80.8%; Score 20.2; DB 4; Length 255;
Best Local Similarity 88.0%; Pred. No. 2.4;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TACCATGAGGACAAATATCATCTG 25
Db 96 TCCGTGAGGCCAAATATCATCTG 120

RESULT 8
US-09-377-497-7
; Sequence 7, Application US/09377497

; Patent No. 6670119
; GENERAL INFORMATION:
; APPLICANT: YOSHIKAWA, YOSHIE
; APPLICANT: MURAI, HIROYUKI
; APPLICANT: ASADA, KIYOZO
; APPLICANT: HINO, FUMITSUGU
; APPLICANT: KATO, IKUNOSHIN
; TITLE OF INVENTION: CANCER-ASSOCIATED GENES
; FILE REFERENCE: 1422-388P
; CURRENT APPLICATION NUMBER: US/09/377,497
; CURRENT FILING DATE: 1999-08-20
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: any n or Xaa = unknown
US-09-377-497-7

Query Match 80.8%; Score 20.2; DB 4; Length 1140;
Best Local Similarity 88.0%; Pred. No. 3.1;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TACCATGAGGACAAATATCATCTG 25
Db 398 TCCGTGAGGCCAAATATCATCTG 422

RESULT 9
US-09-525-906-1
; Sequence 1, Application US/09525906
; Patent No. 6605433
; GENERAL INFORMATION:
; APPLICANT: Jen, Jen
; APPLICANT: Sidransky, David
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Fliss, Makiko
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: Mitochondrial Dosimeter
; FILE REFERENCE: 1107.85815
; CURRENT APPLICATION NUMBER: US/09/525,906
; CURRENT FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 09/377,856
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: 60/097,307
; PRIOR FILING DATE: 1998-08-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 16568
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-525-906-1

Query Match 80.8%; Score 20.2; DB 4; Length 16568;
Best Local Similarity 88.0%; Pred. No. 5.2;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TACCATGAGGACAAATATCATCTG 25
Db 15143 TCCGTGAGGCCAAATATCATCTG 15167

RESULT 10
US-09-097-889-2
; Sequence 2, Application US/09097889
; Patent No. 6218117
; GENERAL INFORMATION:
; APPLICANT: Herrnstadt, Corrina
; APPLICANT: Ghosh, Soumitra S.

APPLICANT: Davis, Robert E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
TITLE OF INVENTION: AGENTS THAT QUANTITATIVELY ALTER DETECTABLE
TITLE OF INVENTION: EXTRAMITOCHONDRIAL DNA: MITOCHONDRIAL DNA RATIOS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/097,889
FILING DATE: 15-JUN-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rosenman Ph.D., Stephen J.
REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 660088.417
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 16569 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-097-889-2

Query Match 80.8%; Score 20.2; DB 3; Length 16569;
Best Local Similarity 88.0%; Pred. No. 5.2;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCACTCTG 25
Db 15144 TCCCGTGAGGCCAAATATCACTCTG 15168

RESULT 11
US-09-377-856-1
Sequence 1, Application US/09377856
Patent No. 6344322
GENERAL INFORMATION:
APPLICANT: Polyak, Kornelia
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: Subtle Mitochondrial Mutations as Tumor
FILE OF INVENTION: Markers
FILE REFERENCE: 1107.82346
CURRENT APPLICATION NUMBER: US/09/377,856
CURRENT FILING DATE: 1999-08-20
PRIOR APPLICATION NUMBER: 60/097,307
PRIOR FILING DATE: 1998-08-20
NUMBER OF SEQ ID NOS: 1
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 16569
TYPE: DNA
ORGANISM: Homo sapiens
US-09-377-856-1

Query Match 80.8%; Score 20.2; DB 3; Length 16569;
Best Local Similarity 88.0%; Pred. No. 5.2;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCACTCTG 25

Db 15144 TCCCGTGAGGCCAAATATCACTCTG 15168

RESULT 12
US-09-302-681-2
Sequence 2, Application US/09302681
Patent No. 6441149
GENERAL INFORMATION:
APPLICANT: HerinStadt, Corrina
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Clevenger, William
APPLICANT: Fahy, Bojin F.
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: DIAGNOSTIC METHOD BASED ON
TITLE OF INVENTION: QUANTIFICATION OF EXTRAMITOCHONDRIAL DNA
FILE REFERENCE: 660088.416C1
CURRENT APPLICATION NUMBER: US/09/302,681
CURRENT FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 108
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 16569
TYPE: DNA
ORGANISM: Homo sapien
US-09-302-681-2

Query Match 80.8%; Score 20.2; DB 4; Length 16569;
Best Local Similarity 88.0%; Pred. No. 5.2;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCACTCTG 25
Db 15144 TCCCGTGAGGCCAAATATCACTCTG 15168

RESULT 13
US-09-098-079-2
Sequence 2, Application US/09098079
Patent No. 6489095
GENERAL INFORMATION:
APPLICANT: HerinStadt, Corrina
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Clevenger, William
APPLICANT: Fahy, Bojin F.
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: DIAGNOSTIC METHOD BASED ON QUANTIFICATION OF
TITLE OF INVENTION: EXTRAMITOCHONDRIAL DNA
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/098,079
FILING DATE: 15-JUN-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rosenman Ph.D., Stephen J.
REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 660088.416
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:

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;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 16569 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; US-09-098-079-2
;
; Query Match      80.8%; Score 20.2; DB 4; Length 16569;
; Best Local Similarity 88.0%; Pred. No. 5.2;
; Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
;
Qy 1 TACCATGAGGACAAATATCATTTCTG 25
Db 15144 TCCCGTGAGGCCAAATATCATTTCTG 15168

RESULT 14
US-10-053-611-1
; Sequence 1, Application US/10053611
; Patent No. 6756021
; GENERAL INFORMATION:
; APPLICANT: Polyak, Kornelia
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: Subtle Mitochondrial Mutations as Tumor
; TITLE OF INVENTION: Markers
; FILE REFERENCE: 1107.82346
; CURRENT APPLICATION NUMBER: US/10/053.611
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US/09/377,856
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: 60/097,307
; PRIOR FILING DATE: 1998-08-20
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 16569
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-053-611-1
;
; Query Match      80.8%; Score 20.2; DB 4; Length 16569;
; Best Local Similarity 88.0%; Pred. No. 5.2;
; Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
;
Qy 1 TACCATGAGGACAAATATCATTTCTG 25
Db 15144 TCCCGTGAGGCCAAATATCATTTCTG 15168

RESULT 15
US-07-825-959-8/c
; Sequence 8, Application US/07825959
; Patent No. 5372929
; GENERAL INFORMATION:
; APPLICANT: Cimino, George C.
; APPLICANT: Lin, Lily
; TITLE OF INVENTION: METHOD FOR MEASURING THE INACTIVATION OF
; TITLE OF INVENTION: PATHOGENS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Limbach & Limbach
; STREET: 2001 Ferry Building
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: US/07/825,959
; FILING DATE: 19920127
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Weseman, James C
; REGISTRATION NUMBER: 30,507
; REFERENCE/DOCKET NUMBER: HRI-02200
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 433-4150
; TELEFAX: (415) 433-8716
; TELEX: 278356
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 34 base pairs
;   TYPE: NUCLEIC ACID
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   FRAGMENT TYPE: internal
; US-07-825-959-8
;
; Query Match      80.0%; Score 20; DB 1; Length 34;
; Best Local Similarity 100.0%; Pred. No. 2;
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
Qy 6 TGAGGACAAATATCATTTCTG 25
Db 34 TGAGGACAAATATCATTTCTG 15

Search completed: November 17, 2004, 03:15:09
Job time : 12.891 secs
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 16:25:24 ; Search time 42.4054 Seconds
(without alignments)
3218.578 Million cell updates/sec

Title: US-09-821-782E-2

Perfect score: 26

Sequence: 1 cctcctagtgttagggattgatcg 26

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_23Sep04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	100.0	26	8 ABQ83298	Abq83298 Cytochrom
2	26	100.0	472	8 ABQ83306	Abq83306 Mitochond
3	26	100.0	472	8 ABQ83307	Abq83307 Mitochond
4	24.4	93.8	200	8 ABX44247	Abx44247 Bovine ES
5	24.4	93.8	235	8 ABX38797	Abx38797 Bovine ES
6	24.4	93.8	241	8 ABX40252	Abx40252 Bovine ES
7	24.4	93.8	331	8 ABX38833	Abx38833 Bovine ES
8	24.4	93.8	411	8 ABX46901	Abx46901 Bovine ES
9	24.4	93.8	416	8 ABX44048	Abx44048 Bovine ES
10	24.4	93.8	417	8 ABX47842	Abx47842 Bovine ES
11	24.4	93.8	419	8 ABX37167	Abx37167 Bovine ES
12	24.4	93.8	448	8 ABX43592	Abx43592 Bovine ES
13	24.4	93.8	469	8 ABX35993	Abx35993 Bovine ES
14	24.4	93.8	472	8 ABQ83314	Abq83314 Mitochond
15	24.4	93.8	472	8 ABQ83313	Abq83313 Mitochond
16	24.4	93.8	472	8 ABQ83327	Abq83327 Mitochond
17	24.4	93.8	472	8 ABQ83296	Abq83296 Antelope
18	24.4	93.8	472	8 ABQ83317	Abq83317 Mitochond
19	24.4	93.8	472	8 ABQ83321	Abq83321 Mitochond
20	24.4	93.8	472	8 ABQ83332	Abq83332 Mitochond
21	24.4	93.8	472	8 ABQ83329	Abq83329 Mitochond

c 22	24.4	93.8	472	8	ABQ83328	Abq83328 Mitochond
c 23	24.4	93.8	472	8	ABQ83303	Abq83303 Mitochond
c 24	24.4	93.8	472	8	ABQ83304	Abq83304 Mitochond
c 25	24.4	93.8	472	8	ABQ83326	Abq83326 Mitochond
c 26	24.4	93.8	472	8	ABQ83337	Abq83337 Mitochond
c 27	24.4	93.8	475	8	ABX40046	Abx40046 Bovine ES
c 28	24.4	93.8	979	6	ABN74229	Abn74229 Bovine em
c 29	22.8	87.7	136	3	AAA43716	Aaa43716 Human sec
c 30	22.8	87.7	210	10	ACD93024	ACD93024 Human col
c 31	22.8	87.7	234	6	ABL37235	ABL37235 Human col
c 32	22.8	87.7	310	10	ACD92164	ACD92164 Human col
c 33	22.8	87.7	320	5	ABV08925	ABV08925 Human pro
c 34	22.8	87.7	347	5	ABV12642	ABv12642 Human pro
c 35	22.8	87.7	351	10	ACD92416	ACD92416 Human col
c 36	22.8	87.7	361	4	AAI82841	Aai82841 Human pol
c 37	22.8	87.7	400	4	AAI87354	Aai87354 Human pol
c 38	22.8	87.7	414	4	AAI87787	Aai87787 Human pol
c 39	22.8	87.7	419	10	ACD93031	ACD93031 Human col
c 40	22.8	87.7	421	4	AAI88933	Aai88933 Human pol
c 41	22.8	87.7	421	9	ACH18049	Ach18049 Human adu
c 42	22.8	87.7	425	4	AAI87673	Aai87673 Human pol
c 43	22.8	87.7	433	6	ABV95467	ABv95467 Human pan
c 44	22.8	87.7	434	4	AAI81714	Aai81714 Human pan
c 45	22.8	87.7	469	6	ABV95916	ABv95916 Human pan

ALIGNMENTS

RESULT 1
ABQ83298
ID ABQ83298 standard; DNA; 26 BP.
XX
AC ABQ83298;
XX
DT 18-JAN-2003 (first entry)
XX
DE Cytochrome b gene universal PCR primer mcb 369 SEQ ID NO:3.
XX
KW Mitochondrial cytochrome b gene; mitochondrial; cytochrome b;
KW identification; criminal investigation; animal poaching; PCR primer; ss.
XX
OS Synthetic.
XX
PN W0200277278-A1.
XX
PD 03-OCT-2002.
XX
PF 28-MAR-2001; 2001WO-IN000055.
XX
PR 28-MAR-2001; 2001WO-IN000055.
XX
(COUL) COUNCIL SCI & IND RES.
XX
PA Verma SK, Singh L;
XX
PI WPI; 2003-018945/01.
XX
PT New universal primers, mcb 398 and mcb 869, capable of amplifying a
PT fragment of cytochrome b gene of any animal species, useful for
PT establishing the identity of biological materials and animals for
PT molecular evidence in forensics.
XX
PS Claim 1; Page 116; 128pp; English.
XX
CC The present invention describes universal primers, mcb 398 and mcb 869
CC (see ABQ83297 and ABQ83298), capable of amplifying a fragment of
CC cytochrome b gene of any animal species in polymerase chain reaction
CC (PCR) and revealing the identity of the biological material of any animal
CC of unknown origin at species and sub-species level. Also described is a
CC method for the identification of the animal from a biological sample. The
CC method is used for animal identification to establish the crime with the
CC criminal beyond a reasonable doubt, to establish the identity of

CC biological materials such as skin, horns confiscated from animal
 CC poachers, if it is that of an endangered species, for the purpose of
 CC molecular evidence of animal hunting and related crime in the court of
 CC law, so that human violation of the wildlife resources could be
 CC controlled, to have an idea of the geographical location of the
 CC commitment of wildlife crime based on the cytochrome b gene haplotype of
 CC poached animal identified by the universal primer invented, to detect the
 CC adulteration of animal meat in food products for the purpose of food
 CC fortification, by the food fortification agencies, to provide a universal
 CC technique for detection of the origin of blood or blood stains collected
 CC from the scene of the crime related to offenses such as murder and rape,
 CC in order to establish the origin of blood found at the scene of the crime
 CC when it sounds as if criminals intentionally spread the blood of an
 CC animal at the scene of the crime to confuse the crime investigators and
 CC forensic scientists with human blood, and so that the method can be
 CC converted to a commercial molecular kit and DNA chips based applications
 CC for wildlife identification in forensics
 XX
 SQ Sequence 26 BP; 4 A; 5 C; 7 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 26; DB 8; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTGTTAGGGATTGATCG 26
 |||||
 DB 1 CCTCCTAGTTGTTAGGGATTGATCG 26

RESULT 2
 ABQ83306/c
 ID ABQ83306 standard; DNA; 472 BP.
 XX
 AC ABQ83306;
 XX
 DT 18-JAN-2003 (first entry)
 XX
 DE Mitochondrial cytochrome b gene sequence SEQ ID NO:11.
 XX
 KW Mitochondrial cytochrome b gene; mitochondrial; cytochrome b;
 KW identification; criminal investigation; animal poaching; gene; ds.
 XX
 OS Unidentified.
 XX
 PN WO200277278-A1.
 XX
 PD 03-OCT-2002.
 XX
 PF 28-MAR-2001; 2001WO-IN000055.
 XX
 PR 28-MAR-2001; 2001WO-IN000055.
 XX
 PA (COUL) COUNCIL SCI & IND RES.
 XX
 PI Verma SK, Singh L;
 XX
 DR WPI; 2003-018945/01.
 XX

PT New universal primers, mcb 398 and mcb 869, capable of amplifying a
 PT fragment of cytochrome b gene of any animal species, useful for
 PT establishing the identity of biological materials and animals for
 PT molecular evidence in forensics.
 XX

PS Example 1; Page 28-57; 128pp; English.

XX The present invention describes universal primers, mcb 398 and mcb 869
 CC (see ABQ83297 and ABQ83298), capable of amplifying a fragment of
 CC cytochrome b gene of any animal species in polymerase chain reaction
 CC (PCR) and revealing the identity of the biological material of any animal
 CC of unknown origin at species and sub-species level. Also described is a
 CC method for the identification of the animal from a biological sample. The
 CC method is used for animal identification to establish the crime with the
 CC criminal beyond a reasonable doubt, to establish the identity of

CC biological materials such as skin, horns confiscated from animal
 CC poachers, if it is that of an endangered species, for the purpose of
 CC molecular evidence of animal hunting and related crime in the court of
 CC law, so that human violation of the wildlife resources could be
 CC controlled, to have an idea of the geographical location of the
 CC commitment of wildlife crime based on the cytochrome b gene haplotype of
 CC poached animal identified by the universal primer invented, to detect the
 CC adulteration of animal meat in food products for the purpose of food
 CC fortification, by the food fortification agencies, to provide a universal
 CC technique for detection of the origin of blood or blood stains collected
 CC from the scene of the crime related to offenses such as murder and rape,
 CC in order to establish the origin of blood found at the scene of the crime
 CC when it sounds as if criminals intentionally spread the blood of an
 CC animal at the scene of the crime to confuse the crime investigators and
 CC forensic scientists with human blood, and so that the method can be
 CC converted to a commercial molecular kit and DNA chips based applications
 CC for wildlife identification in forensics. The present sequence represents
 CC a mitochondrial cytochrome b gene sequence from the present invention
 XX
 SQ Sequence 472 BP; 140 A; 153 C; 66 G; 113 T; 0 U; 0 Other;

Query Match 100.0%; Score 26; DB 8; Length 472;
 Best Local Similarity 100.0%; Pred. No. 0.034;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTGTTAGGGATTGATCG 26
 |||||
 DB 472 CCTCCTAGTTGTTAGGGATTGATCG 447

RESULT 3
 ABQ83307/c
 ID ABQ83307 standard; DNA; 472 BP.
 XX
 AC ABQ83307;
 XX
 DT 18-JAN-2003 (first entry)
 XX
 DE Mitochondrial cytochrome b gene sequence SEQ ID NO:12.
 XX
 KW Mitochondrial cytochrome b gene; mitochondrial; cytochrome b;
 KW identification; criminal investigation; animal poaching; gene; ds.
 XX
 OS Unidentified.
 XX
 PN WO200277278-A1.
 XX
 PD 03-OCT-2002.
 XX
 PF 28-MAR-2001; 2001WO-IN000055.
 XX
 PR 28-MAR-2001; 2001WO-IN000055.
 XX
 PA (COUL) COUNCIL SCI & IND RES.
 XX
 PI Verma SK, Singh L;
 XX
 DR WPI; 2003-018945/01.
 XX

PT New universal primers, mcb 398 and mcb 869, capable of amplifying a
 PT fragment of cytochrome b gene of any animal species, useful for
 PT establishing the identity of biological materials and animals for
 PT molecular evidence in forensics.
 XX

PS Example 1; Page 28-57; 128pp; English.

XX The present invention describes universal primers, mcb 398 and mcb 869
 CC (see ABQ83297 and ABQ83298), capable of amplifying a fragment of
 CC cytochrome b gene of any animal species in polymerase chain reaction
 CC (PCR) and revealing the identity of the biological material of any animal
 CC of unknown origin at species and sub-species level. Also described is a
 CC method for the identification of the animal from a biological sample. The
 CC method is used for animal identification to establish the crime with the
 CC method is used for animal identification to establish the crime with the

CC criminal beyond a reasonable doubt, to establish the identity of
 CC biological materials such as skin, horns confiscated from animal
 CC poachers, if it is that of an endangered species, for the purpose of
 CC molecular evidence of animal hunting and related crime in the court of
 CC law, so that human violation of the wildlife resources could be
 CC controlled, to have an idea of the geographical location of the
 CC commitment of wildlife crime based on the cytochrome b gene haplotype of
 CC poached animal identified by the universal primer invented, to detect the
 CC adulteration of animal meat in food products for the purpose of food
 CC fortification, by the food fortification agencies, to provide a universal
 CC technique for detection of the origin of blood or blood stains collected
 CC from the scene of the crime related to offenses such as murder and rape,
 CC in order to establish the origin of blood found at the scene of the crime
 CC when it sounds as if criminals intentionally spread the blood of an
 CC animal at the scene of the crime to confuse the crime investigators and
 CC forensic scientists with human blood, and so that the method can be
 CC converted to a commercial molecular kit and DNA chips based applications
 CC for wildlife identification in forensics. The present sequence represents
 CC a mitochondrial cytochrome b gene sequence from the present invention
 XX
 XX Sequence 472 BP; 141 A; 153 C; 66 G; 112 T; 0 U; 0 Other;

Query Match 100.0%; Score 26; DB 8; Length 472;
 Best Local Similarity 100.0%; Pred. No. 0.034;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTTGTAGGGATTGATCG 26
 DB 472 CCTCCTAGTTTGTAGGGATTGATCG 447

RESULT 4
 ABX44247/c
 ID ABX44247 standard; cDNA; 200 BP.

XX AC ABX44247;
 XX
 XX 21-FEB-2003 (first entry)
 XX
 XX Bovine EST associated with lactation/muscle/fat deposition #9412.
 DE
 XX Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
 KW muscle deposition; fat deposition; genome mapping; gene identification;
 KW gene analysis; cattle breeding.
 XX
 XX Bos Taurus.
 XX
 XX US2002137139-A1.
 XX
 XX 26-SEP-2002.
 XX
 XX 24-SEP-2001; 2001US-00960352.
 XX
 XX 12-JAN-1999; 99US-0115707P.
 XX
 XX 11-JAN-2000; 2000US-00480902.
 XX
 XX (BYAT/) BYATT J C.
 XX (MATH/) MATHIALAGAN N.
 XX (TAON/) TAO N.
 XX (WARR/) WARREN W C.
 XX
 XX Byatt JC, Mathialagan N, Tao N, Warren WC;
 XX WPI; 2003-110599/10.
 XX
 XX New nucleic acid associated with lactation, and muscle and fat
 PT deposition, useful for genome mapping, gene identification and analysis,
 PT cattle breeding, or for genetically improving cattle.
 XX
 XX Claim 2; SEQ ID NO 9412; 245pp; English.
 XX
 XX The invention relates to a purified nucleic acid molecule associated with
 CC lactation or muscle and fat deposition (designated LMFD), derived from

CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
 CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
 CC appearing as ABX34836-ABX49947, or complements of them. Also included are
 CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
 CC acid linked to a promoter and a 3' non- translated sequence that
 CC functions in the cell to cause termination of transcription and addition
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
 CC (2) determining a level or pattern of a molecule in a bovine cell or
 CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
 CC of the 15112 nucleic acid sequences or its complement or fragment) with a
 CC complementary nucleic acid molecule obtained from the bovine cell or
 CC tissue, where hybridisation between the marker nucleic acid and the
 CC complementary nucleic acid permits the detection of the molecule; and (b)
 CC detecting the level or pattern of the complementary nucleic acid, where
 CC the detection of the complementary nucleic acid is predictive of the
 CC level or pattern of the molecule. The LMFD nucleic acid is used for
 CC determining a level or pattern of a molecule in a bovine cell or tissue.
 CC It is useful for genome mapping, gene identification and analysis, cattle
 CC breeding, preparation of constructs for use in cattle gene expression, or
 CC for genetically improving cattle. The present sequence is one of the
 CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
 CC present sequence was not shown in the specification but was obtained in
 CC electronic format from the USPTO web site:
 CC seqdata.uspto.gov/sequence.html?DocID=20020137139
 XX

SQ Sequence 200 BP; 62 A; 66 C; 28 G; 44 T; 0 U; 0 Other;

Query Match 93.8%; Score 24.4; DB 8; Length 200;
 Best Local Similarity 96.2%; Pred. No. 0.17;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTTGTAGGGATTGATCG 26
 DB 36 CCTCCTAGTTTGTAGGGATTGATCG 11

RESULT 5
 ABX38797/c

ID ABX38797 standard; cDNA; 235 BP.

XX AC ABX38797;
 XX
 XX 20-FEB-2003 (first entry)
 XX
 XX Bovine EST associated with lactation/muscle/fat deposition #3962.
 DE
 XX Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
 KW muscle deposition; fat deposition; genome mapping; gene identification;
 KW gene analysis; cattle breeding.
 XX
 XX Bos Taurus.
 XX
 XX US2002137139-A1.
 XX
 XX 26-SEP-2002.
 XX
 XX 24-SEP-2001; 2001US-00960352.
 XX
 XX 12-JAN-1999; 99US-0115707P.
 XX
 XX 11-JAN-2000; 2000US-00480902.
 XX
 XX (BYAT/) BYATT J C.
 XX (MATH/) MATHIALAGAN N.
 XX (TAON/) TAO N.
 XX (WARR/) WARREN W C.
 XX
 XX Byatt JC, Mathialagan N, Tao N, Warren WC;
 XX WPI; 2003-110599/10.
 XX
 XX New nucleic acid associated with lactation, and muscle and fat
 PT deposition, useful for genome mapping, gene identification and analysis,
 PT cattle breeding, or for genetically improving cattle.

XX PS Claim 2; SEQ ID NO 3962; 245pp; English.

XX CC The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non-translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising: (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid, where the detection of the complementary nucleic acid is predictive of the level or pattern of the molecule. The LMFD nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle breeding, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site: seqdata.uspto.gov/sequence.html?DocID=20020137139

XX SQ Sequence 235 BP; 76 A; 76 C; 27 G; 56 T; 0 U; 0 Other;

Query Match 93.8%; Score 24.4; DB 8; Length 235;
Best Local Similarity 96.2%; Pred. No. 0.18; Mismatches 1; Indels 0; Gaps 0;
Matches 25; Conservative 0;

Oy 1 CCTCTAGTTGTTAGGGATTGATCG 26
|||||
Db 144 CCTCTAGTTGTTAGGGATTGATCG 119
|||||

RESULT 6
ABX40252/c
ID ABX40252 standard; cDNA; 241 BP.

XX AC ABX40252;

XX DT 20-FEB-2003 (first entry)

XX DE Bovine EST associated with lactation/muscle/fat deposition #5417.

XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
KW muscle deposition; fat deposition; genome mapping; gene identification;
KW gene analysis; cattle breeding.

XX OS Bos Taurus.

XX US2002137139-A1.

XX PD 26-SEP-2002.

XX PF 24-SEP-2001; 2001US-00960352.

XX PR 12-JAN-1999; 99US-0115707P.

XX PR 11-JAN-2000; 2000US-00480902.

XX PA (BYATT/) BYATT J C.

XX PA (MATH/) MATHIALAGAN N.

XX PA (TAON/) TAO N.

XX PA (WARR/) WARREN W C.

XX PI Byatt JC, Mathialagan N, Tao N, Warren WC;

XX

DR WPI; 2003-110599/10.

XX PT New nucleic acid associated with lactation, and muscle and fat deposition, useful for genome mapping, gene identification and analysis, cattle breeding, or for genetically improving cattle.

XX PS Claim 2; SEQ ID NO 5417; 245pp; English.

XX CC The invention relates to a purified nucleic acid molecule associated with lactation or muscle and fat deposition (designated LMFD), derived from cattle, and the LMFD nucleic acid can specifically hybridise to a second nucleic acid molecule comprising any of 15112 nucleotide sequences, appearing as ABX34836-ABX49947, or complements of them. Also included are (1) a transformed cell having a nucleic acid comprising an LMFD nucleic acid linked to a promoter and a 3' non-translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and (2) determining a level or pattern of a molecule in a bovine cell or tissue comprising: (a) incubating a marker nucleic acid (comprising any of the 15112 nucleic acid sequences or its complement or fragment) with a complementary nucleic acid molecule obtained from the bovine cell or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule; and (b) detecting the level or pattern of the complementary nucleic acid, where the detection of the complementary nucleic acid is predictive of the level or pattern of the molecule. The LMFD nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle breeding, preparation of constructs for use in cattle gene expression, or for genetically improving cattle. The present sequence is one of the 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site: seqdata.uspto.gov/sequence.html?DocID=20020137139

XX SQ Sequence 241 BP; 75 A; 82 C; 27 G; 57 T; 0 U; 0 Other;

Query Match 93.8%; Score 24.4; DB 8; Length 241;
Best Local Similarity 96.2%; Pred. No. 0.18; Mismatches 1; Indels 0; Gaps 0;
Matches 25; Conservative 0;

Oy 1 CCTCTAGTTGTTAGGGATTGATCG 26
|||||
Db 96 CCTCTAGTTGTTAGGGATTGATCG 71
|||||

RESULT 7
ABX38833/c
ID ABX38833 standard; cDNA; 331 BP.

XX AC ABX38833;

XX DT 20-FEB-2003 (first entry)

XX DE Bovine EST associated with lactation/muscle/fat deposition #3998.

XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
KW muscle deposition; fat deposition; genome mapping; gene identification;
KW gene analysis; cattle breeding.

XX OS Bos Taurus.

XX US2002137139-A1.

XX PD 26-SEP-2002.

XX PF 24-SEP-2001; 2001US-00960352.

XX PR 12-JAN-1999; 99US-0115707P.

XX PR 11-JAN-2000; 2000US-00480902.

XX PA (BYATT/) BYATT J C.

XX PA (MATH/) MATHIALAGAN N.

PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 XX
 PI Byatt JC, Mathialagan N, Tao N, Warren WC;
 XX
 DR WPI; 2003-110599/10.
 XX
 XX New nucleic acid associated with lactation, and muscle and fat
 PT deposition, useful for genome mapping, gene identification and analysis,
 PT cattle breeding, or for genetically improving cattle.
 XX
 PS Claim 2; SEQ ID NO 3998; 245pp; English.
 XX
 CC The invention relates to a purified nucleic acid molecule associated with
 CC lactation or muscle and fat deposition (designated LMFD), derived from
 CC cattle, and the LMFD nucleic acid can specifically hybridize to a second
 CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
 CC appearing as ABX34836-ABX49947, or complements of them. Also included are
 CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
 CC acid linked to a promoter and a 3' non-translated sequence that
 CC functions in the cell to cause termination of transcription and addition
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
 CC (2) determining a level or pattern of a molecule in a bovine cell or
 CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
 CC of the 15112 nucleic acid sequences or its complement or fragment) with a
 CC complementary nucleic acid molecule obtained from the bovine cell or
 CC tissue, where hybridisation between the marker nucleic acid and the
 CC complementary nucleic acid permits the detection of the molecule; and (b)
 CC detecting the level or pattern of the complementary nucleic acid, where
 CC the detection of the complementary nucleic acid is predictive of the
 CC level or pattern of the molecule. The LMFD nucleic acid is used for
 CC determining a level or pattern of a molecule in a bovine cell or tissue.
 CC It is useful for genome mapping, gene identification and analysis, cattle
 CC breeding, preparation of constructs for use in cattle gene expression, or
 CC for genetically improving cattle. The present sequence is one of the
 CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
 CC present sequence was not shown in the specification but was obtained in
 CC electronic format from the USPTO web site:
 CC seqdata.uspto.gov/sequence.html?DocID=20020137139
 XX
 SQ Sequence 331 BP; 101 A; 107 C; 48 G; 75 T; 0 U; 0 Other;
 Query Match 93.8%; Score 24.4; DB 8; Length 331;
 Best Local Similarity 96.2%; Pred. No. 0.19;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 CCTCCTAGTTGTTAGGGATTGATCG 26
 Db 78 CCTCCTAGTTGTTAGGGATTGATCG 53
 RESULT 8
 ABX46901/c
 ID ABX46901 standard; cDNA; 411 BP.
 XX
 AC ABX46901;
 XX
 XX 21-FEB-2003 (first entry)
 DT
 DE Bovine EST associated with lactation/muscle/fat deposition #12066.
 XX
 KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
 KW muscle deposition; fat deposition; genome mapping; gene identification;
 KW gene analysis; cattle breeding.
 XX
 OS Bos Taurus.
 XX
 XX US2002137139-A1.
 PN
 XX 26-SEP-2002.
 PD
 XX 24-SEP-2001; 2001US-00960352.
 PF
 XX

PR 12-JAN-1999; 99US-0115707P.
 PR 11-JAN-2000; 2000US-00480902.
 XX
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 XX
 PI Byatt JC, Mathialagan N, Tao N, Warren WC;
 XX
 DR WPI; 2003-110599/10.
 XX
 XX New nucleic acid associated with lactation, and muscle and fat
 PT deposition, useful for genome mapping, gene identification and analysis,
 PT cattle breeding, or for genetically improving cattle.
 XX
 PS Claim 2; SEQ ID NO 12066; 245pp; English.
 XX
 CC The invention relates to a purified nucleic acid molecule associated with
 CC lactation or muscle and fat deposition (designated LMFD), derived from
 CC cattle, and the LMFD nucleic acid can specifically hybridize to a second
 CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
 CC appearing as ABX34836-ABX49947, or complements of them. Also included are
 CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
 CC acid linked to a promoter and a 3' non-translated sequence that
 CC functions in the cell to cause termination of transcription and addition
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
 CC (2) determining a level or pattern of a molecule in a bovine cell or
 CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
 CC of the 15112 nucleic acid sequences or its complement or fragment) with a
 CC complementary nucleic acid molecule obtained from the bovine cell or
 CC tissue, where hybridisation between the marker nucleic acid and the
 CC complementary nucleic acid permits the detection of the molecule; and (b)
 CC detecting the level or pattern of the complementary nucleic acid, where
 CC the detection of the complementary nucleic acid is predictive of the
 CC level or pattern of the molecule. The LMFD nucleic acid is used for
 CC determining a level or pattern of a molecule in a bovine cell or tissue.
 CC It is useful for genome mapping, gene identification and analysis, cattle
 CC breeding, preparation of constructs for use in cattle gene expression, or
 CC for genetically improving cattle. The present sequence is one of the
 CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
 CC present sequence was not shown in the specification but was obtained in
 CC electronic format from the USPTO web site:
 CC seqdata.uspto.gov/sequence.html?DocID=20020137139
 XX
 SQ Sequence 411 BP; 133 A; 138 C; 53 G; 87 T; 0 U; 0 Other;
 Query Match 93.8%; Score 24.4; DB 8; Length 411;
 Best Local Similarity 96.2%; Pred. No. 0.19;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 CCTCCTAGTTGTTAGGGATTGATCG 26
 Db 135 CCTCCTAGTTGTTAGGGATTGATCG 110
 RESULT 9
 ABX44048/c
 ID ABX44048 standard; cDNA; 416 BP.
 XX
 AC ABX44048;
 XX
 XX 21-FEB-2003 (first entry)
 DT
 DE Bovine EST associated with lactation/muscle/fat deposition #9213.
 XX
 KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
 KW muscle deposition; fat deposition; genome mapping; gene identification;
 KW gene analysis; cattle breeding.
 XX
 OS Bos Taurus.
 XX
 XX US2002137139-A1.
 PN

XX 26-SEP-2002.
 XX
 XX
 PF 24-SEP-2001; 2001US-00960352.
 XX
 XX
 PR 12-JAN-1999; 99US-0115707P.
 PR 11-JAN-2000; 2000US-00480902.
 XX
 XX
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 XX
 PI Byatt JC, Mathialagan N, Tao N, Warren WC;
 XX WPI; 2003-110599/10.
 XX
 XX
 PT New nucleic acid associated with lactation, and muscle and fat
 PT deposition, useful for genome mapping, gene identification and analysis,
 PT cattle breeding, or for genetically improving cattle.
 XX
 XX
 PS Claim 2; SEQ ID NO 9213; 245pp; English.
 XX
 CC The invention relates to a purified nucleic acid molecule associated with
 CC lactation or muscle and fat deposition (designated LMFD), derived from
 CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
 CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
 CC appearing as ABX34836-ABX49947, or complements of them. Also included are
 CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
 CC acid linked to a promoter and a 3' non- translated sequence that
 CC functions in the cell to cause termination of transcription and addition
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
 CC (2) determining a level or pattern of a molecule in a bovine cell or
 CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
 CC of the 15112 nucleic acid sequences or its complement or fragment) with a
 CC complementary nucleic acid molecule obtained from the bovine cell or
 CC tissue, where hybridisation between the marker nucleic acid and the
 CC complementary nucleic acid permits the detection of the molecule; and (b)
 CC detecting the level or pattern of the complementary nucleic acid, where
 CC the detection of the complementary nucleic acid is predictive of the
 CC level or pattern of the molecule. The LMFD nucleic acid is used for
 CC determining a level or pattern of a molecule in a bovine cell or tissue.
 CC It is useful for genome mapping, gene identification and analysis, cattle
 CC breeding, preparation of constructs for use in cattle gene expression, or
 CC for genetically improving cattle. The present sequence is one of the
 CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
 CC present sequence was not shown in the specification but was obtained in
 CC electronic format from the USPTO web site:
 CC seqdata.uspto.gov/sequence.html?DocID=20020137139
 XX
 SQ Sequence 416 BP; 138 A; 132 C; 57 G; 89 T; 0 U; 0 Other;
 Query Match 93.8%; Score 24.4; DB 8; Length 416;
 Best Local Similarity 96.2%; Pred. No. 0.19;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 CCTCCTAGTTGTTAGGATTGATCG 26
 |||||
 DB 115 CCTCCTAGTTGTTAGGATTGATCG 90
 |||||
 RESULT 10
 ABX47842/c
 ID ABX47842 standard; cDNA; 417 BP.
 XX
 XX ABX47842;
 XX
 XX
 DT 21-FEB-2003 (first entry)
 XX
 XX Bovine EST associated with lactation/muscle/fat deposition #13007.
 XX
 XX Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
 KW muscle deposition; fat deposition; genome mapping; gene identification;

KW gene analysis; cattle breeding.
 XX
 OS Bos Taurus.
 XX
 FN US2002137139-A1.
 XX
 PD 26-SEP-2002.
 XX
 XX
 PF 24-SEP-2001; 2001US-00960352.
 XX
 PR 12-JAN-1999; 99US-0115707P.
 PR 11-JAN-2000; 2000US-00480902.
 XX
 XX
 PA (BYAT/) BYATT J C.
 PA (MATH/) MATHIALAGAN N.
 PA (TAON/) TAO N.
 PA (WARR/) WARREN W C.
 XX
 PI Byatt JC, Mathialagan N, Tao N, Warren WC;
 XX WPI; 2003-110599/10.
 XX
 XX
 PT New nucleic acid associated with lactation, and muscle and fat
 PT deposition, useful for genome mapping, gene identification and analysis,
 PT cattle breeding, or for genetically improving cattle.
 XX
 XX
 PS Claim 2; SEQ ID NO 13007; 245pp; English.
 XX
 CC The invention relates to a purified nucleic acid molecule associated with
 CC lactation or muscle and fat deposition (designated LMFD), derived from
 CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
 CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
 CC appearing as ABX34836-ABX49947, or complements of them. Also included are
 CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
 CC acid linked to a promoter and a 3' non- translated sequence that
 CC functions in the cell to cause termination of transcription and addition
 CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
 CC (2) determining a level or pattern of a molecule in a bovine cell or
 CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
 CC of the 15112 nucleic acid sequences or its complement or fragment) with a
 CC complementary nucleic acid molecule obtained from the bovine cell or
 CC tissue, where hybridisation between the marker nucleic acid and the
 CC complementary nucleic acid permits the detection of the molecule; and (b)
 CC detecting the level or pattern of the complementary nucleic acid, where
 CC the detection of the complementary nucleic acid is predictive of the
 CC level or pattern of the molecule. The LMFD nucleic acid is used for
 CC determining a level or pattern of a molecule in a bovine cell or tissue.
 CC It is useful for genome mapping, gene identification and analysis, cattle
 CC breeding, preparation of constructs for use in cattle gene expression, or
 CC for genetically improving cattle. The present sequence is one of the
 CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
 CC present sequence was not shown in the specification but was obtained in
 CC electronic format from the USPTO web site:
 CC seqdata.uspto.gov/sequence.html?DocID=20020137139
 XX
 SQ Sequence 417 BP; 137 A; 138 C; 53 G; 89 T; 0 U; 0 Other;
 Query Match 93.8%; Score 24.4; DB 8; Length 417;
 Best Local Similarity 96.2%; Pred. No. 0.19;
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 CCTCCTAGTTGTTAGGATTGATCG 26
 |||||
 DB 152 CCTCCTAGTTGTTAGGATTGATCG 127
 |||||
 RESULT 11
 ABX37167/c
 ID ABX37167 standard; cDNA; 419 BP.
 XX
 XX ABX37167;
 XX
 XX 20-FEB-2003 (first entry)
 DT

XX DE Bovine EST associated with lactation/muscle/fat deposition #2332.
XX AC
XX XX
XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
KW muscle deposition; fat deposition; genome mapping; gene identification;
KW gene analysis; cattle breeding.
XX OS
XX Bos Taurus.
XX XX
XX PN US2002137139-A1.
XX XX
XX PD 26-SEP-2002.
XX XX
XX PF 24-SEP-2001; 2001US-00960352.
XX XX
XX PR 12-JAN-1999; 99US-0115707P.
XX PR 11-JAN-2000; 2000US-00480902.
XX XX
XX PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
XX XX
XX PI Byatt JC, Mathialagan N, Tao N, Warren WC;
XX WPI; 2003-110599/10.
XX XX
XX PT New nucleic acid associated with lactation, and muscle and fat
PT deposition, useful for genome mapping, gene identification and analysis,
PT cattle breeding, or for genetically improving cattle.
XX XX
XX PS Claim 2; SEQ ID NO 2332; 245pp; English.
XX XX
XX CC The invention relates to a purified nucleic acid molecule associated with
CC lactation or muscle and fat deposition (designated LMFD), derived from
CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
CC appearing as ABX34836-ABX49947, or complements of them. Also included are
CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
CC acid linked to a promoter and a 3' non- translated sequence that
CC functions in the cell to cause termination of transcription and addition
CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
CC (2) determining a level or pattern of a molecule in a bovine cell or
CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
CC of the 15112 nucleic acid sequences or its complement or fragment) with a
CC complementary nucleic acid molecule obtained from the bovine cell or
CC tissue, where hybridisation between the marker nucleic acid and the
CC complementary nucleic acid permits the detection of the molecule; and
CC detecting the level or pattern of the complementary nucleic acid, where
CC the detection of the complementary nucleic acid is predictive of the
CC level or pattern of the molecule. The LMFD nucleic acid is used for
CC determining a level or pattern of a molecule in a bovine cell or tissue.
CC It is useful for genome mapping, gene identification and analysis, cattle
CC breeding, preparation of constructs for use in cattle gene expression, or
CC for genetically improving cattle. The present sequence is one of the
CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
CC present sequence was not shown in the specification but was obtained in
CC electronic format from the USPTO web site:
CC seqdata.uspto.gov/sequence.html?DocID=20020137139
XX XX
XX SQ Sequence 419 BP; 123 A; 141 C; 53 G; 102 T; 0 U; 0 Other;

Query Match 93.8%; Score 24.4; DB 8; Length 419;
Best Local Similarity 96.2%; Pred. No. 0.19;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTGTTAGGGATTGATCG 26
|||||
Db 194 CCTCCTAGTTGTTAGGGATTGATCG 169
|||||

RESULT 12
ABX43592/c

ID ABX43592 standard; cDNA; 448 BP.
XX AC
XX XX
XX XX
XX DT 21-FEB-2003 (first entry)
XX KW Bovine EST associated with lactation/muscle/fat deposition #8757.
XX DE
XX XX
XX KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
KW muscle deposition; fat deposition; genome mapping; gene identification;
KW gene analysis; cattle breeding.
XX OS
XX Bos Taurus.
XX XX
XX PN US2002137139-A1.
XX XX
XX PD 26-SEP-2002.
XX XX
XX PF 24-SEP-2001; 2001US-00960352.
XX XX
XX PR 12-JAN-1999; 99US-0115707P.
XX PR 11-JAN-2000; 2000US-00480902.
XX XX
XX PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
XX XX
XX PI Byatt JC, Mathialagan N, Tao N, Warren WC;
XX WPI; 2003-110599/10.
XX XX
XX PT New nucleic acid associated with lactation, and muscle and fat
PT deposition, useful for genome mapping, gene identification and analysis,
PT cattle breeding, or for genetically improving cattle.
XX XX
XX PS Claim 2; SEQ ID NO 8757; 245pp; English.
XX XX
XX CC The invention relates to a purified nucleic acid molecule associated with
CC lactation or muscle and fat deposition (designated LMFD), derived from
CC cattle, and the LMFD nucleic acid can specifically hybridise to a second
CC nucleic acid molecule comprising any of 15112 nucleotide sequences,
CC appearing as ABX34836-ABX49947, or complements of them. Also included are
CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
CC acid linked to a promoter and a 3' non- translated sequence that
CC functions in the cell to cause termination of transcription and addition
CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
CC (2) determining a level or pattern of a molecule in a bovine cell or
CC tissue comprising: (a) incubating a marker nucleic acid (comprising any
CC of the 15112 nucleic acid sequences or its complement or fragment) with a
CC complementary nucleic acid molecule obtained from the bovine cell or
CC tissue, where hybridisation between the marker nucleic acid and the
CC complementary nucleic acid permits the detection of the molecule; and
CC detecting the level or pattern of the complementary nucleic acid, where
CC the detection of the complementary nucleic acid is predictive of the
CC level or pattern of the molecule. The LMFD nucleic acid is used for
CC determining a level or pattern of a molecule in a bovine cell or tissue.
CC It is useful for genome mapping, gene identification and analysis, cattle
CC breeding, preparation of constructs for use in cattle gene expression, or
CC for genetically improving cattle. The present sequence is one of the
CC 15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
CC present sequence was not shown in the specification but was obtained in
CC electronic format from the USPTO web site:
CC seqdata.uspto.gov/sequence.html?DocID=20020137139
XX XX
XX SQ Sequence 448 BP; 131 A; 146 C; 55 G; 116 T; 0 U; 0 Other;

Query Match 93.8%; Score 24.4; DB 8; Length 448;
Best Local Similarity 96.2%; Pred. No. 0.19;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTCCTAGTTGTTAGGGATTGATCG 26
|||||
|||||

Query Match 93.8%; Score 24.4; DB 8; Length 469;

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 22:24:28 ; Search time 343.642 Seconds
(without alignments)
2650.992 Million cell updates/sec

Title: US-09-821-782E-1

Perfect score: 25

Sequence: 1 taccatgagacaaatattcttg 25

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1.*
2: gb_est2.*
3: gb_btc.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	130	6	CB219995 1Abo10D11
2	25	100.0	315	6	CB060285 4010439 B
3	25	100.0	328	7	CF615703 CES014188
4	25	100.0	338	1	AU277825 AU277825
5	25	100.0	361	4	BM430528 1Duo35F3
6	25	100.0	398	2	BE589920 196607 BA
7	25	100.0	398	4	BG688078 335513 BA
8	25	100.0	408	4	BM433056 1JBJ9D3.a
9	25	100.0	411	5	BP112175 BP112175
10	25	100.0	413	4	BM433038 1JBJ9B6.a
11	25	100.0	414	6	CB225030 1OM28R03
12	25	100.0	431	5	BP110134 BP110134
13	25	100.0	432	1	AV613710 AV613710
14	25	100.0	432	1	AV663157 AV663157
15	25	100.0	436	6	CB060174 4010727 B
16	25	100.0	438	2	BF430396 934 MARC
17	25	100.0	442	2	BE483891 170238 BA
18	25	100.0	442	6	CB220057 1Abo16G09
19	25	100.0	442	7	CN791814 4126609 B
20	25	100.0	445	2	BF429564 1105 MARC
21	25	100.0	446	2	BF429555 1095 MARC
22	25	100.0	448	2	BF429532 1068 MARC
23	25	100.0	448	6	CB221459 1Duo11H10
24	25	100.0	453	5	BP112710 BP112710

25	100.0	456	7	CN432453	CN432453 BE0200010
26	100.0	462	4	BM480699	BM480699 531379 MA
27	100.0	467	7	CN822416	CN822416 Oa_spln
28	100.0	468	2	BF604803	BF604803 270971 MA
29	100.0	477	4	BM430220	BM430220 1Duo31D6
30	100.0	479	5	BP110300	BP110300 BP110300
31	100.0	482	7	CF931047	CF931047 CF--06-R-
32	100.0	483	4	BM432066	BM432066 1JBJ16A10
33	100.0	484	4	BM445456	BM445456 11L11F12
34	100.0	484	6	CB220685	CB220685 1Abo25C08
35	100.0	484	6	CB223613	CB223613 1JBJ25F2
36	100.0	485	2	BF889654	BF889654 289202 MA
37	100.0	485	6	CB224011	CB224011 1JBJ30D2
38	100.0	486	6	CB221941	CB221941 11L21H5 B
39	100.0	487	4	BM434623	BM434623 1R111A03
40	100.0	489	2	BF652253	BF652253 275762 MA
41	100.0	490	6	CB221081	CB221081 1Abo30A09
42	100.0	491	6	CB223477	CB223477 1JBJ23H6
43	100.0	492	4	BM429985	BM429985 1Duo28A12
44	100.0	493	6	CB222631	CB222631 11L30B01
45	100.0	496	5	BP110116	BP110116 BP110116

ALIGNMENTS

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CB219995
LOCUS 1Abo10D11 Bos taurus Abomasum #1 library Bos taurus CDNA, mRNA linear EST 10-FEB-2003
DEFINITION sequence.
ACCESSION CB219995
VERSION CB219995.1 GI:28290509
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 130)
AUTHORS Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Sensen, C.W., Gordon, P.M.K. and Moore, S.S.
TITLE Gene Expression Profiling of the Bovine Gastrointestinal Tract
JOURNAL Unpublished (2002)
COMMENT Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
Tel: 780 492 0169
Fax: 780 492 4265
Email: stephen.moore@ualberta.ca
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FEATURES
source Location/Qualifiers
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/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="Smooth muscle"
/cell_type="Epithelial"
/dev_stage="Young adult"
/lab_host="X11-BlueMRF"-strain"
/clone_lib="Bos taurus Abomasum #1 library"
/note="Organ: Abomasum; Vector: Uni-2ZAPXR; Site_1: EcoR I; Site_2: Xho I"

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Best Local Similarity 100.0%; Pred. No. 0.89;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TACCATGAGCAAAATATCATTCGT 25
|||||

Db 52 TACCATGAGGACAAATATCATCTG 76

RESULT 2

CB060285/c

LOCUS

DEFINITION

4010439 BARC-EMBRAPA 326BOV Bos indicus cDNA clone 326BOV_1005

ACCESSION

CB060285

VERSION

CB060285.1

KEYWORDS

EST.

SOURCE

ORGANISM

Bos indicus (zebu)

REFERENCE

AUTHORS

1 (bases 1 to 315)

da Mota, A.F., Sonstegard, T.S., Van Tassel, C.P., Matukumalli, L.K.,

Wood, D.L., Capuco, A.V., Brito, M.A.P., Martinez, M.L., Connor, E.E.,

Machado, M.A. and Coutinho, L.L.

Construction and Characterization of cDNA Libraries Generated from

Mammary Gland Tissues of Holstein (Bos taurus) and Gir (Bos

indicus) Cattle

Unpublished (2002)

Contact: Adilson F. da Mota

Gene Evaluation and Mapping Laboratory

USDA, ARS, Animal and Natural Resources Institute

Blsg. 200 Rm3 BARC-East, Beltsville, MD 20705, USA

Tel: 3015048456

Fax: 3015048414

Email: amota@npgl.embrrapa.br

Single pass sequencing. Bases called and trimmed with phred

0.000925 using options -trim alt - -trim fasta. Vector identified

by cross_match using options -mismatch 12 -mismatch 12

PCR Primers

FORWARD: GTTTCCAGTCACGAGTTG

BACKWARD: TGAGCGGATAACATTTTCACACAG

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Seq primer: GTTTTCCAGTCACGAGTTG

High quality sequence stop: 315.

Location/Qualifiers

1..315

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/mol_type="mRNA"

/strain="Brazilian Dairy Gir"

/db_xref="taxon:9915"

/clone="326BOV_1005"

/sex="female"

/tissue_type="parenchyma"

/cell_type="epithelium"

/dev_stage="involved"

/lab_host="DH5alpha"

/clone_lib="BARC-EMBRAPA 326BOV"

/note="Organ: mammary; Vector: pUC 118; Site 1: HincII;

Site 2: HincII; This mammary-derived cDNA library was

created as part of a collaborative project between the ARS

Gene Evaluation and Mapping Laboratory and the EMBRAPA

Dairy Cattle Research Center under the sponsorship of

USDA, ARS/EMBRAPA-LABEX program in animal genomics. RNA

sample from cow AM1, samples 2, 4, and 5 extracted on

3/27/02, RT with Superscript II at 37 deg C annealing

temperature, PCR with 16-mers."

ORIGIN

Query Match

Best Local Similarity

Matches

25; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

RESULT 3

CF615703

LOCUS

DEFINITION

CF615703

ACCESSION

CF615703

VERSION

CF615703.1

KEYWORDS

EST.

SOURCE

ORGANISM

Bos taurus (cow)

REFERENCE

AUTHORS

1 (bases 1 to 328)

Wang, Y.H., Byrne, K., Vuocolo, T., Tan, S.H., McWilliam, S., Dierens, L.

and Lehnert, S.

Transcription profiling of bovine skeletal muscle and subcutaneous

fat

Unpublished (2003)

Contact: Dr Sigrd Lehnert

Functional Genomics Lab

CSIRO Livestock Industries

Level 5, Queensland Bioscience Precinct, University of Queensland,

306 Carmody Road St Lucia QLD Australia

Tel: 07 3214 2445

Fax: 07 3214 2480

Email: Sigrd.Lehnert@csiro.au

Plate: 12 row: H column: 05.

Location/Qualifiers

1..328

/organism="Bos taurus"

/mol_type="mRNA"

/strain="Angus"

/db_xref="taxon:9913"

/clone="CCL013263"

/sex="male"

/tissue_type="Longissimus dorsi muscle"

/dev_stage="Young Adult"

/lab_host="XLI-BlueMRF'strain"

/clone_lib="Bos taurus muscle cDNA library"

/note="Organ: skeletal muscle; Vector: Uni-ZAPXR; Site 1:

Scor1; Site 2: Xho I; Library made from skeletal muscle of

a 14 month old Angus steer."

ORIGIN

Query Match

Best Local Similarity

Matches

25; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

CF615703

LOCUS

DEFINITION

CF615703

ACCESSION

CF615703

VERSION

CF615703.1

KEYWORDS

EST.

SOURCE

ORGANISM

Bos taurus (cow)

REFERENCE

AUTHORS

1 (bases 1 to 328)

Wang, Y.H., Byrne, K., Vuocolo, T., Tan, S.H., McWilliam, S., Dierens, L.

and Lehnert, S.

Transcription profiling of bovine skeletal muscle and subcutaneous

fat

Unpublished (2003)

Contact: Dr Sigrd Lehnert

Functional Genomics Lab

CSIRO Livestock Industries

Level 5, Queensland Bioscience Precinct, University of Queensland,

306 Carmody Road St Lucia QLD Australia

Tel: 07 3214 2445

Fax: 07 3214 2480

Email: Sigrd.Lehnert@csiro.au

Plate: 12 row: H column: 05.

Location/Qualifiers

1..328

/organism="Bos taurus"

/mol_type="mRNA"

/strain="Angus"

/db_xref="taxon:9913"

/clone="CCL013263"

/sex="male"

/tissue_type="Longissimus dorsi muscle"

/dev_stage="Young Adult"

/lab_host="XLI-BlueMRF'strain"

/clone_lib="Bos taurus muscle cDNA library"

/note="Organ: skeletal muscle; Vector: Uni-ZAPXR; Site 1:

Scor1; Site 2: Xho I; Library made from skeletal muscle of

a 14 month old Angus steer."

ORIGIN

Query Match

Best Local Similarity

Matches

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0; Mismatches

0; Indels

0; Gaps

0;

RESULT 4

CF615703

LOCUS

DEFINITION

CF615703

ACCESSION

CF615703

VERSION

CF615703.1

KEYWORDS

EST.

SOURCE

ORGANISM

Bos taurus (cow)

REFERENCE

AUTHORS

1 (bases 1 to 338)

Oishi, M., Yamada, T., Goma, H., Lejukole, H.Y., Taniguchi, Y. and

Sasaki, Y.

EST analysis of cloned bovine fetus and placenta

Unpublished (2002)

Contact: Masahito Oishi

Location/Qualifiers

1..338

/organism="Bos taurus"

/mol_type="mRNA"

/strain="Angus"

/db_xref="taxon:9913"

/clone="CCL013263"

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/tissue_type="Longissimus dorsi muscle"

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/lab_host="XLI-BlueMRF'strain"

/clone_lib="Bos taurus muscle cDNA library"

/note="Organ: skeletal muscle; Vector: Uni-ZAPXR; Site 1:

Scor1; Site 2: Xho I; Library made from skeletal muscle of

a 14 month old Angus steer."

ORIGIN

Query Match

Best Local Similarity

Matches

25; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

CF615703

LOCUS

DEFINITION

CF615703

ACCESSION

CF615703

VERSION

CF615703.1

KEYWORDS

EST.

SOURCE

ORGANISM

Bos taurus (cow)

REFERENCE

AUTHORS

1 (bases 1 to 338)

Oishi, M., Yamada, T., Goma, H., Lejukole, H.Y., Taniguchi, Y. and

Sasaki, Y.

EST analysis of cloned bovine fetus and placenta

Unpublished (2002)

Contact: Masahito Oishi

Location/Qualifiers

1..338

/organism="Bos taurus"

/mol_type="mRNA"

/strain="Angus"

/db_xref="taxon:9913"

/clone="CCL013263"

/sex="male"

/tissue_type="Longissimus dorsi muscle"

/dev_stage="Young Adult"

/lab_host="XLI-BlueMRF'strain"

/clone_lib="Bos taurus muscle cDNA library"

/note="Organ: skeletal muscle; Vector: Uni-ZAPXR; Site 1:

Scor1; Site 2: Xho I; Library made from skeletal muscle of

a 14 month old Angus steer."

ORIGIN

Query Match

Best Local Similarity

Matches

25; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

RESULT 5

CF615703

LOCUS

DEFINITION

CF615703

Graduate School of Agriculture
Kyoto University
Sakyoku Kitashirakawa, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-6331
Fax: 81-75-753-6340
Email: oishi@kajs.jkns.kais.kyoto-u.ac.jp.

FEATURES

source

1. .338
Location/Qualifiers
/organism="Bos taurus"
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/clone_lib="Cloned bovine fetus cdna"

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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 230 TACCATGAGGACAAATATCATCTG 206

RESULT 5

LOCUS

BM430528 361 bp mRNA linear EST 31-JAN-2002
1Du035F3.abl Bos taurus Duodenum #1 library Bos taurus cdna, mRNA
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Bos taurus (cow)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
Tel: 780 492 0169
Fax: 780 492 4265
Email: stephen.moore@ualberta.ca
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FEATURES

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/cell_type="Simple columnar epithelial"
/dev_stage="Young adult"
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/clone_lib="Bos taurus Duodenum #1 library"
/note="Organ: Intestine/duodenum; Vector: Uni-22APXR;
Site_1: EcoRI; Site_2: Xho I"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 10 TACCATGAGGACAAATATCATCTG 34

RESULT 6

LOCUS

BE589920 398 bp mRNA linear EST 27-MAR-2003
196607 BARC 5BOV Bos taurus cdna 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Bos taurus (cow)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

1 (bases 1 to 398)
Sonstegard, T., Capuco, A.V., White, J., Van Tassel, C.P.,
Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
and Quackenbush, J.
Analysis of bovine mammary gland EST and functional annotation of
the Bos taurus gene index
Mamm. Genome 13 (7), 373-379 (2002)
12135956
12140684

Contact: Sonstegard TS
USDA, ARS, Beltsville Agricultural Research Center
Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
Tel: 301 504 8416
Fax: 301 504 8414

Email: tads@psi.barc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACACGCTATGACCAT
BACKWARD: GTTTCCCGAGTCACGACG
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Seq primer: ATTAGTGACACTATAG.

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/clone_lib="BARC 5BOV"
/note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
Library made from pooled mRNA isolated from mammary
tissues at eight physiological, developmental, and disease
states."

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Best Local Similarity 100.0%; Pred. No. 1;
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DB 370 TACCATGAGGACAAATATCATCTG 394

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BG688078 398 bp mRNA linear EST 27-MAR-2003
335513 BARC 5BOV Bos taurus cdna 5', mRNA sequence.

DEFINITION BG688078
ACCESSION BG688078
VERSION BG688078.1 GI:13929879
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.

REFERENCE 1 (bases 1 to 398)

AUTHORS
 Sonstegard, T., Capuco, A.V., White, J., Van Tassell, C.P.,
 Connor, E.E., Cho, J., Sultana, R., Shade, L., Wray, J.E., Wells, K.D.
 and Quackenbush, J.

TITLE
 Analysis of bovine mammary gland EST and functional annotation of
 the Bos taurus gene index

**JOURNAL
 MEDLINE
 PUBMED**
 Mamm. Genome 13 (7), 373-379 (2002)
 22135956
 12140684

COMMENT
 Contact: Sonstegard TS
 USDA, ARS, Beltsville Agricultural Research Center
 Bldg. 200 Rm 2A, Beltsville, MD 20705, USA
 Tel: 301 504 8416
 Fax: 301 504 8414
 Email: tads@psi.barc.usda.gov
 Single pass sequencing. Bases called and alt trimmed with phred
 v0.980904.e. Vector identified by cross_match with the -minscore 18
 and -minmatch 12 options.
 PCR Primers
 FORWARD: AGGAACAGCTATGACCAT
 BACKWARD: GTTTCACGTCACGCG
 Plate: 34 row: I column: 18
 Seq primer: ATTTAGGTGACACTATAG.
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 /tissue_type="pooled"
 /lab_host="DH10B"
 /clone_lib="BARC 5B0V"
 /note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
 Library made from pooled mRNA isolated from mammary
 tissues at eight physiological, developmental, and disease
 states."

FEATURES
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 Query Match 100.0%; Score 25; DB 4; Length 398;
 Best Local Similarity 100.0%; Pred. No. 1;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN
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 Db 374 TACCATGAGGACAAATATCATCTG 398
 |||||

RESULT 8
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 LOCUS 408 bp mRNA linear EST 31-JAN-2002
 DEFINITION 1JF9D3.ab1 Bos taurus Jejenum #1 library Bos taurus cDNA, mRNA
 sequence.
 ACCESSION BM433056
 VERSION BM433056.1 GI:18454778
 KEYWORDS EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.

REFERENCE
 1 (bases 1 to 408)
 Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Senses, C.W.,
 Gordon, P.M.K. and Moore, S.S.
 Gene Expression Profiling of the Bovine Gastrointestinal Tract
 Unpublished (2002)
 Contact: Dr. Stephen Moore
 Beef Genomics Laboratory
 Dept of AFNS, University of Alberta
 410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
 Tel: 780 492 0169
 Fax: 780 492 4265
 Email: stephen.moore@ualberta.ca
 Insert Length: 408 Std Error: 0.00
 POLYA=yes.
 Location/Qualifiers

FEATURES
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 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FEATURES
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 Db 330 TACCATGAGGACAAATATCATCTG 354
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RESULT 9
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 DEFINITION BP112175 ORCS bovine utero-placenta cDNA Bos taurus cDNA clone
 ORCS12814 5', mRNA sequence.
 ACCESSION BP112175
 VERSION BP112175.1 GI:28314465
 KEYWORDS EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.

REFERENCE
 1 (bases 1 to 411)
 Ishiwata, H., Katsuma, S., Kizaki, K., Patel, O.V., Nakano, H.,
 Takahashi, T., Imai, K., Hirasawa, A., Shiojima, S., Ikawa, H.,
 Suzuki, Y., Tsujimoto, G., Izaiki, Y., Todoroki, J., and Hashizume, K.
 Characterization of gene expression profiles in early bovine
 pregnancy using a custom cDNA microarray
 Mol. Reprod. Dev. 65 (1), 9-18 (2003)
 22544902
 12658628
 Contact: Gozoh Tsujimoto
 Department of Molecular, Cell Pharmacology
 National Research Institute for Child Health and Development
 3-35-31 Taishido, Setagaya, Tokyo 154-8567, Japan
 Tel: 81-3-3149-2476
 Fax: 81-3-3149-1252
 Email: gtsujimoto@nch.go.jp
 This work was performed to collaborate with Developmental Biology
 Department, National Institute of Agrobiological Sciences. Address:
 2 Ikenodai, Tsukuba, Ibaraki, 305-8602 Japan. Phone & Fax:
 81-29-838-8633 e-mail: kazuha@affrc.go.jp
 This work was funded by Organized Research Combination System
 (ORCS) project of Ministry of Education, Culture, Sports, Science
 and Technology.
 Location/Qualifiers
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ORIGIN
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 /note="Organ: Intestine/Jejunum; Vector: Uni-2ZAPXR;
 Site 1: EcoRI; Site 2: Xho I"

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 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 9

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 DEFINITION BP112175 ORCS bovine utero-placenta cDNA Bos taurus cDNA clone
 ORCS12814 5', mRNA sequence.

ACCESSION BP112175
VERSION BP112175.1 GI:28314465
KEYWORDS EST.

SOURCE Bos taurus (cow)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.

REFERENCE

1 (bases 1 to 411)
 Ishiwata, H., Katsuma, S., Kizaki, K., Patel, O.V., Nakano, H.,
 Takahashi, T., Imai, K., Hirasawa, A., Shiojima, S., Ikawa, H.,
 Suzuki, Y., Tsujimoto, G., Izaiki, Y., Todoroki, J., and Hashizume, K.
 Characterization of gene expression profiles in early bovine
 pregnancy using a custom cDNA microarray
 Mol. Reprod. Dev. 65 (1), 9-18 (2003)
 22544902

PUBMED 12658628

COMMENT

Contact: Gozoh Tsujimoto
 Department of Molecular, Cell Pharmacology
 National Research Institute for Child Health and Development
 3-35-31 Taishido, Setagaya, Tokyo 154-8567, Japan
 Tel: 81-3-3149-2476
 Fax: 81-3-3149-1252
 Email: gtsujimoto@nch.go.jp

This work was performed to collaborate with Developmental Biology
 Department, National Institute of Agrobiological Sciences. Address:
 2 Ikenodai, Tsukuba, Ibaraki, 305-8602 Japan. Phone & Fax:
 81-29-838-8633 e-mail: kazuha@affrc.go.jp
 This work was funded by Organized Research Combination System
 (ORCS) project of Ministry of Education, Culture, Sports, Science
 and Technology.

FEATURES

Location/Qualifiers

1. 411
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 /clone_lib="ORCS bovine utero-placenta cDNA"

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 DEFINITION
 1 JEU9B6.ab1 Bos taurus Jejenum #1 library Bos taurus cDNA, mRNA
 sequence.
 BM433038
 VERSION
 BM433038.1 GI:18454760
 KEYWORDS
 EST.
 SOURCE
 Bos taurus (cow)
 ORGANISM
 Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.
 REFERENCE
 1 (bases 1 to 413)
 Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Sensen, C.W.,
 Gordon, P.M.K. and Moore, S.S.
 Gene Expression Profiling of the Bovine Gastrointestinal Tract
 Unpublished (2002)
 JOURNAL
 COMMENT
 Contact: Dr. Stephen Moore
 Beef Genomics Laboratory
 Dept of AFNS, University of Alberta
 410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
 Tel: 780 492 0169
 Fax: 780 492 4265
 Email: stephen.moore@ualberta.ca
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 /clone_lib="Bos taurus Jejenum #1 library"
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 Db 372 TACCATGAGGACAAATATCATCTG 396
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RESULT 11
 CB225030
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 DEFINITION
 10M28B03 Bos taurus Omasum #1 library Bos taurus cDNA, mRNA
 sequence.
 CB225030
 VERSION
 CB225030.1 GI:28295544
 KEYWORDS
 EST.
 SOURCE
 Bos taurus (cow)
 ORGANISM
 Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.
 REFERENCE
 1 (bases 1 to 414)
 Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Sensen, C.W.,
 Gordon, P.M.K. and Moore, S.S.
 Gene Expression Profiling of the Bovine Gastrointestinal Tract
 Unpublished (2002)
 JOURNAL

COMMENT
 Contact: Dr. Stephen Moore
 Beef Genomics Laboratory
 Dept of AFNS, University of Alberta
 410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
 Tel: 780 492 0169
 Fax: 780 492 4265
 Email: stephen.moore@ualberta.ca
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 Site_2: Xho I"

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 Db 183 TACCATGAGGACAAATATCATCTG 207
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RESULT 12
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 LOCUS
 DEFINITION
 BP110134 ORCS bovine utero-placenta cDNA Bos taurus cDNA clone
 ORCS10131 5', mRNA sequence.
 BP110134
 ACCESSION
 BP110134.1 GI:28312422
 VERSION
 EST.
 KEYWORDS
 SOURCE
 Bos taurus (cow)
 ORGANISM
 Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.
 REFERENCE
 1 (bases 1 to 431)
 Ishiwata, H., Katsuma, S., Kiraki, K., Patel, O.V., Nakano, H.,
 Takahashi, T., Imai, K., Hirasawa, A., Shiojima, S., Ikawa, H.,
 Suzuki, Y., Tsujimoto, G., Izaike, Y., Todoroki, J. and Hashizume, K.
 Characterization of gene expression profiles in early bovine
 pregnancy using a custom cDNA microarray
 Mol. Reprod. Dev. 65 (1), 9-18 (2003)
 22544902
 12658628
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT
 Contact: Gozoh Tsujimoto
 Department of Molecular, Cell Pharmacology
 National Research Institute for Child Health and Development
 3-35-31 Taishido, Setagaya, Tokyo 154-8567, Japan
 Tel: 81-3-3149-2476
 Fax: 81-3-3149-1252
 Email: gtsujimoto@nch.go.jp
 This work was performed to collaborate with Developmental Biology
 Department, National Institute of Agrobiological Sciences. Address:
 2 Ikenodai, Tsukuba, Ibaraki, 305-8602 Japan. Phone & Fax:
 81-29-839-8633 e-mail: kazuna@affrc.go.jp
 This work was funded by Organized Research Combination System
 (ORCS) project of Ministry of Education, Culture, Sports, Science
 and Technology.

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Db 373 TACCATGAGGACAAATATCATCTG 397

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LOCUS
DEFINITION AV613710 Bos taurus adipocyte cell line Bos taurus cDNA clone
E0AD009D01 5', mRNA sequence.
ACCESSION AV613710
VERSION AV613710.1 GI:9749380
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
REFERENCE 1 (bases 1 to 432)
AUTHORS Takasuga,A., Hirotsune,S., Itoh,R., Jitohzono,A., Suzuki,H., Aso,H.
and Sugimoto,Y.
TITLE Establishment of a high throughput EST sequencing system using
poly(A) tail-removed cDNA libraries and determination of 36,000
bovine ESTs
JOURNAL Nucleic Acids Res. 29 (22), E108 (2001)
MEDLINE 21570554
PUBMED 11713328
COMMENT Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5641
Fax: 81-248-25-5725
Email: kazusugi@cococ.ocn.ne.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
FEATURES
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LOCUS
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Unknown, mRNA sequence.
ACCESSION CB060174
VERSION CB060174.1 GI:27798461
KEYWORDS EST.
SOURCE Bos indicus (zebu)
ORGANISM Bos indicus
REFERENCE 1 (bases 1 to 436)
AUTHORS da Mota,A.F., Sonstegard,T.S., Van Tassel,C.P., Matukumalli,L.K.,
Wood,B.L., Capuco,A.V., Brito,M.A.P., Martinez,M.L., Connor,E.E.,
Machado,M.A. and Coutinho,L.L.
TITLE Construction and Characterization of cDNA Libraries Generated from
Mammary Gland Tissues of Holstein (Bos taurus) and Gir (Bos
indicus) Cattle
JOURNAL Unpublished (2002)
COMMENT Contact: Adilson F. da Mota
Gene Evaluation and Mapping Laboratory
USDA, ARS, Animal and Natural Resources Institute
Bldg. 200 Rm3 BARC-East, Beltsville, MD 20705, USA

```

Tel: 3015048456
Fax: 3015048414
Email: amota@cnpg1.embrapa.br
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim alt '' -trim fasta. Vector identified
by cross match using options -mismatch 12 -minscore 12
PCR PRIMERs
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BACKWARD: TGACGGATACAAATTCACACAG
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 Site 2: HincII; This mammary-derived cDNA library was
 created as part of a collaborative project between the ARS
 Gene Evaluation and Mapping Laboratory and the EMBRAPA
 Dairy Cattle Research Center under the sponsorship of
 USDA, ARS/EMBRAPA-LABEX program in animal genomics. RNA
 sample from cow AML, samples 2, 4, and 5 extracted on
 3/27/02, RT with Superscript II at 37 deg C annealing
 temperature, PCR with 16-mers."

ORIGIN

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Search completed: November 17, 2004, 02:10:47
Job time : 349.642 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 23:47:45 ; Search time 37.2849 Seconds
(without alignments)

3621.431 Million cell updates/sec

Title: US-09-821-782E-1

Perfect score: 25

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum DE seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	25	100.0	380	9	US-09-960-352-7247
5	25	100.0	388	9	US-09-960-352-1396
6	25	100.0	397	9	US-09-960-352-7805
7	25	100.0	402	9	US-09-960-352-12218
8	25	100.0	409	9	US-09-960-352-4672
9	25	100.0	409	9	US-09-960-352-7414
10	25	100.0	409	9	US-09-960-352-9374
11	25	100.0	411	9	US-09-960-352-8498
12	25	100.0	412	9	US-09-960-352-1120

13	25	100.0	413	9	US-09-960-352-2257	Sequence 2257, Ap
14	25	100.0	414	9	US-09-960-352-11264	Sequence 11264, A
15	25	100.0	415	9	US-09-960-352-5186	Sequence 5186, Ap
16	25	100.0	417	9	US-09-960-352-7034	Sequence 7034, Ap
17	25	100.0	417	9	US-09-960-352-10703	Sequence 10703, A
18	25	100.0	419	9	US-09-960-352-2976	Sequence 2976, Ap
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22	25	100.0	422	9	US-09-960-352-12981	Sequence 12981, A
23	25	100.0	424	9	US-09-960-352-5146	Sequence 5146, Ap
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25	25	100.0	428	9	US-09-960-352-5221	Sequence 5221, Ap
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27	25	100.0	432	9	US-09-960-352-7281	Sequence 7281, Ap
28	25	100.0	433	9	US-09-960-352-12794	Sequence 12794, A
29	25	100.0	435	9	US-09-960-352-9656	Sequence 9656, Ap
30	25	100.0	436	9	US-09-960-352-1774	Sequence 1774, Ap
31	25	100.0	443	9	US-09-960-352-8234	Sequence 8234, Ap
32	25	100.0	444	9	US-09-960-352-5945	Sequence 5945, Ap
33	25	100.0	445	9	US-09-960-352-10147	Sequence 10147, A
34	25	100.0	446	9	US-09-960-352-12797	Sequence 12797, A
35	25	100.0	446	9	US-09-960-352-13262	Sequence 13262, A
36	25	100.0	447	9	US-09-960-352-4014	Sequence 4014, Ap
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38	25	100.0	448	9	US-09-960-352-2970	Sequence 2970, Ap
39	25	100.0	455	9	US-09-960-352-3957	Sequence 3957, Ap
40	25	100.0	458	9	US-09-960-352-3753	Sequence 3753, Ap
41	25	100.0	474	13	US-10-079-623-151	Sequence 151, App
42	25	100.0	483	9	US-09-960-352-8523	Sequence 8523, Ap
43	25	100.0	910	11	US-09-876-143-1475	Sequence 1475, Ap
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45	25	100.0	970	11	US-09-876-143-1697	Sequence 1697, Ap

ALIGNMENTS

RESULT 1
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; Sequence 14288, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 14288
; LENGTH: 329
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 61-LIB058-015-Q1-K1-H10
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Best Local Similarity 100.0%; Pred. No. 0.19; Mismatches 0; Indels 0; Gaps 0;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-09-960-352-6557
; Sequence 6557, Application US/09960352
; Patent No. US20020137139A1

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; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 6557
; LENGTH: 346
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 28-LIB34-007-Q1-E1-G7
US-09-960-352-6557

Query Match      100.0%; Score 25; DB 9; Length 346;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
Db 174 TACCATGAGGACAAATATCATCTG 198

RESULT 3
US-09-960-352-6350
; Sequence 6350, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 6350
; LENGTH: 353
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 27-LIB34-033-Q1-E1-G3
US-09-960-352-6350

Query Match      100.0%; Score 25; DB 9; Length 353;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
Db 324 TACCATGAGGACAAATATCATCTG 348

RESULT 4
US-09-960-352-7247
; Sequence 7247, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
```

```
; SEQ ID NO 7247
; LENGTH: 380
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 31-LIB34-008-Q1-E1-H11
US-09-960-352-7247

Query Match      100.0%; Score 25; DB 9; Length 380;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
Db 174 TACCATGAGGACAAATATCATCTG 198

RESULT 5
US-09-960-352-1396
; Sequence 1396, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 1396
; LENGTH: 388
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (44),(60)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 07-BOVMS1-018-Q1-E1-B3
US-09-960-352-1396

Query Match      100.0%; Score 25; DB 9; Length 388;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
Db 109 TACCATGAGGACAAATATCATCTG 133

RESULT 6
US-09-960-352-7805
; Sequence 7805, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 7805
; LENGTH: 397
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 34-BOVMS1-002-Q1-E1-A6
US-09-960-352-7805
```

```
Query Match      100.0%; Score 25; DB 9; Length 397;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
Db 125 TACCATGAGGACAAATATCATCTG 149

RESULT 7
US-09-960-352-12218
; Sequence 12218, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 12218
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (300)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 52-LIB34-007-Q1-E1-E9
US-09-960-352-12218

Query Match      100.0%; Score 25; DB 9; Length 402;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
Db 309 TACCATGAGGACAAATATCATCTG 333

RESULT 8
US-09-960-352-4672
; Sequence 4672, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 4672
; LENGTH: 409
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 20-LIB34-031-Q1-E1-E7
US-09-960-352-4672

Query Match      100.0%; Score 25; DB 9; Length 409;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
Db 340 TACCATGAGGACAAATATCATCTG 364

RESULT 9
US-09-960-352-7414
; Sequence 7414, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 7414
; LENGTH: 409
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (300)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 32-LIB3057-021-Q1-K1-H7
US-09-960-352-7414

Query Match      100.0%; Score 25; DB 9; Length 409;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
Db 373 TACCATGAGGACAAATATCATCTG 397

RESULT 10
US-09-960-352-9374
; Sequence 9374, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 9374
; LENGTH: 409
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 40-LIB34-028-Q1-E1-B12
US-09-960-352-9374

Query Match      100.0%; Score 25; DB 9; Length 409;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
Db 379 TACCATGAGGACAAATATCATCTG 403

RESULT 11
US-09-960-352-8498
; Sequence 8498, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
```

;
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 8498
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 36-LIB34-071-Q1-E1-A8
US-09-960-352-8498

Query Match 100.0%; Score 25; DB 9; Length 411;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
|||||
DB 378 TACCATGAGGACAAATATCATCTG 402

RESULT 12

US-09-960-352-1120
; Sequence 1120, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:

; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan

; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 1120
; LENGTH: 412
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 05-LIB34-063-Q1-E1-B1
US-09-960-352-1120

Query Match 100.0%; Score 25; DB 9; Length 412;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
|||||
DB 372 TACCATGAGGACAAATATCATCTG 396

RESULT 13

US-09-960-352-2257
; Sequence 2257, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:

; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan

; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 2257
; LENGTH: 413
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 10-LIB34-017-Q1-E1-C5

US-09-960-352-2257

Query Match 100.0%; Score 25; DB 9; Length 413;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
|||||
DB 384 TACCATGAGGACAAATATCATCTG 408

RESULT 14

US-09-960-352-11264
; Sequence 11264, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:

; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan

; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 11264
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 48-LIB34-026-Q1-E1-D8
US-09-960-352-11264

Query Match 100.0%; Score 25; DB 9; Length 414;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
|||||
DB 384 TACCATGAGGACAAATATCATCTG 408

RESULT 15

US-09-960-352-5186
; Sequence 5186, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:

; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan

; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 5186
; LENGTH: 415
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 22-LIB34-073-Q1-E1-F5
US-09-960-352-5186

Query Match 100.0%; Score 25; DB 9; Length 415;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCATCTG 25
|||||
DB 374 TACCATGAGGACAAATATCATCTG 398

Search completed: November 17, 2004, 03:11:49
Job time : 39.2849 secs

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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 16:25:24 ; Search time 769.82 Seconds
(without alignments)
3218.578 Million cell updates/sec

Title: US-09-821-782E-48

Perfect score: 472

Sequence: 1 taccatgagacaatatct.....attcctaacaactaggagg 472

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

1: Geneseqn1980s: *
2: Geneseqn1990s: *
3: Geneseqn2000s: *
4: Geneseqn2001as: *
5: Geneseqn2001bs: *
6: Geneseqn2002as: *
7: Geneseqn2002bs: *
8: Geneseqn2003as: *
9: Geneseqn2003bs: *
10: Geneseqn2003cs: *
11: Geneseqn2003ds: *
12: Geneseqn2004s: *

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	472	100.0	472	8	ABQ83296 Antilope
2	392	83.1	472	8	ABQ83308
3	387.2	82.0	472	8	ABQ83307
4	384	81.4	472	8	ABQ83306
5	384	81.4	472	8	ABQ83321
6	376	79.7	472	8	ABQ83333
7	374.4	79.3	472	8	ABQ83331
8	374.4	79.3	472	8	ABQ83334
9	372.8	79.0	472	8	ABQ83303
10	372.8	79.0	472	8	ABQ83330
11	371.8	78.8	472	8	ABQ83311
12	371.2	78.6	472	8	ABQ83313
13	371.2	78.6	472	8	ABQ83332
14	371.2	78.6	472	8	ABQ83328
15	369.6	78.3	472	8	ABQ83310
16	369.6	78.3	472	8	ABQ83315
17	369.6	78.3	472	8	ABQ83304
18	369.6	78.3	472	8	ABQ83326
19	368	78.0	472	8	ABQ83314
20	368	78.0	472	8	ABQ83322
21	368	78.0	472	8	ABQ83312

22	368	78.0	472	8	ABQ83337	Abq83337 Mitochond
23	367.2	77.8	472	8	ABQ83301	Abq83301 Mitochond
24	365.6	77.5	472	8	ABQ83317	Abq83317 Mitochond
25	364.8	77.3	472	8	ABQ83336	Abq83336 Mitochond
26	364.8	77.3	472	8	ABQ83335	Abq83335 Mitochond
27	363.2	76.9	472	8	ABQ83320	Abq83320 Mitochond
28	361.6	76.6	472	8	ABQ83327	Abq83327 Mitochond
29	361.6	76.6	472	8	ABQ83309	Abq83309 Mitochond
30	361.6	76.6	472	8	ABQ83338	Abq83338 Mitochond
31	360	76.3	472	8	ABQ83319	Abq83319 Mitochond
32	360	76.3	472	8	ABQ83305	Abq83305 Mitochond
33	358.4	75.9	472	8	ABQ83323	Abq83323 Mitochond
34	358.4	75.9	472	8	ABQ83316	Abq83316 Mitochond
35	356.8	75.6	472	8	ABQ83340	Abq83340 Mitochond
36	355.2	75.3	472	8	ABQ83339	Abq83339 Mitochond
37	354.8	75.2	472	8	ABQ83302	Abq83302 Mitochond
38	351.4	74.4	472	8	ABQ83329	Abq83329 Mitochond
39	350	74.2	472	8	ABQ83324	Abq83324 Mitochond
40	347.2	73.6	472	8	ABQ83318	Abq83318 Mitochond
41	345.2	73.1	472	8	ABQ83325	Abq83325 Mitochond
42	321.6	68.1	1144	10	ADB35253	Add5253 Mouse mlt
43	321.6	68.1	3552	2	AAZ77492	Aaz77492 Human ova
44	320	67.8	599	3	AAC86457	Rac86457 Mouse cyt
45	318.4	67.5	16300	10	ADB59175	Adb59175 Toxicity-

ALIGNMENTS

RESULT 1
ABQ83296
ID ABQ83296 standard; DNA; 472 BP.
XX
AC ABQ83296;
XX
DT 18-JAN-2003 (first entry)
XX
DE Antilope cervicapra mitochondrial cytochrome b gene SEQ ID NO:1.
XX
KW Mitochondrial cytochrome b gene; mitochondrial; cytochrome b;
KW identification; criminal investigation; animal poaching;
KW Antilope cervicapra; blackbuck; gene; ds.
XX
OS Antilope cervicapra.
XX
PN WO20027278-A1.
XX
PD 03-OCT-2002.
XX
PF 28-MAR-2001; 2001WO-IN000055.
XX
PR 28-MAR-2001; 2001WO-IN000055.
XX
(COUL) COUNCIL SCI & IND RES.
XX
Verma SK, Singh L;
XX
DR WPI; 2003-018945/01.
XX
New universal primers, mcb 398 and mcb 869, capable of amplifying a
PT fragment of cytochrome b gene of any animal species, useful for
PT establishing the identity of biological materials and animals for
PT molecular evidence in forensics.
XX
Claim 5; Page 116; 128pp; English.
PS
CC The present invention describes universal primers, mcb 398 and mcb 869
CC (see ABQ83297 and ABQ83298), capable of amplifying a fragment of
CC cytochrome b gene of any animal species in polymerase chain reaction
CC of unknown origin at species and sub-species level. Also described is a
CC method for the identification of the animal from a biological sample. The
CC method is used for animal identification to establish the crime with the

CC criminal beyond a reasonable doubt, to establish the identity of
CC biological materials such as skin, horns confiscated from animal
CC poachers, if it is that of an endangered species, for the purpose of
CC molecular evidence of animal hunting and related crime in the court of
CC law, so that human violation of the wildlife resources could be
CC controlled, to have an idea of the geographical location of the
CC commitment of wildlife crime based on the cytochrome b gene haplotype of
CC poached animal identified by the universal primer invented, to detect the
CC adulteration of animal meat in food products for the purpose of food
CC fortification, by the food fortification agencies, to provide a universal
CC technique for detection of the origin of blood or blood stains collected
CC from the scene of the crime related to offenses such as murder and rape,
CC in order to establish the origin of blood found at the scene of the crime
CC when it sounds as if criminals intentionally spread the blood of an
CC animal at the scene of the crime to confuse the crime investigators and
CC forensic scientists with human blood, and so that the method can be
CC converted to a commercial molecular kit and DNA chips based applications
CC for wildlife identification in forensics. The present sequence represents
CC a specifically claimed Antelope cervicapra (blackbuck) mitochondrial
CC cytochrome b gene sequence from the present invention
XX
SQ Sequence 472 BP; 146 A; 145 C; 61 G; 120 T; 0 U; 0 Other;

Query Match 100.0%; Score 472; DB 8; Length 472;
Best Local Similarity 100.0%; Pred. No. 1.5e-137; Indels 0; Gaps 0;
Matches 472; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TACCATGAGGACAAATATCTTTTTCAGGAGCAACAGTATCATCAACCAATCTCTTTTCAGCAA 60
DB 1 TACCATGAGGACAAATATCTTTTTCAGGAGCAACAGTATCATCAACCAATCTCTTTTCAGCAA 60
QY 61 TCCCATATACCGTACCAACCTAGTAGATGAATCTGAGGAGGTTCTCAGTAGATAAG 120
DB 61 TCCCATATACCGTACCAACCTAGTAGATGAATCTGAGGAGGTTCTCAGTAGATAAG 120
QY 121 CAACCTTTACCGGATTTTTCGCTTCCACTTTATCTCTCCATTTATCATTTGAGCCCTTA 180
DB 121 CAACCTTTACCGGATTTTTCGCTTCCACTTTATCTCTCCATTTATCATTTGAGCCCTTA 180
QY 181 CCATAGTACACCTACTGTGTTTCCAGAAACAGGATCCAAACCCCAACAGGAATCTCAT 240
DB 181 CCATAGTACACCTACTGTGTTTCCAGAAACAGGATCCAAACCCCAACAGGAATCTCAT 240
QY 241 CAGACGACAGCAAAATTCATTTCCACCCCTACTACACTATCAAGATATCTTAGAGCTC 300
DB 241 CAGACGACAGCAAAATTCATTTCCACCCCTACTACACTATCAAGATATCTTAGAGCTC 300
QY 301 TACTATTAAATTTAAACCCCTCATGCTTCTAGTCTTATCTTCCCGGACCTGCTTGGAGACC 360
DB 301 TACTATTAAATTTAAACCCCTCATGCTTCTAGTCTTATCTTCCCGGACCTGCTTGGAGACC 360
QY 361 CAGACAACTATACACAGCAAAACCCCACTTAATACACCCCAACATATCAAGCCGAATGAT 420
DB 361 CAGACAACTATACACAGCAAAACCCCACTTAATACACCCCAACATATCAAGCCGAATGAT 420
QY 421 ACTTCCTATTTCATACGCAATCTCCGATCAATTTCTTAACAACTAGGAGG 472
DB 421 ACTTCCTATTTCATACGCAATCTCCGATCAATTTCTTAACAACTAGGAGG 472

RESULT 2
ABQ83308
ID ABQ83308 standard; DNA; 472 BP.
XX
AC ABQ83308;
XX
AC
XX
DT 18-JAN-2003 (first entry)
XX
DE Mitochondrial cytochrome b gene sequence SEQ ID NO:13.
XX
KW Mitochondrial cytochrome b gene; mitochondrial; cytochrome b;
KW identification; criminal investigation; animal poaching; gene; ds.
XX

OS Unidentified.
XX WO200277278-A1.
XX 03-OCT-2002.
XX
XX 28-MAR-2001; 2001WO-IN000055.
XX
XX 28-MAR-2001; 2001WO-IN000055.
XX
XX (COUL) COUNCIL SCI & IND RES.
XX
XX Verma SK, Singh L;
XX WPI; 2003-018945/01.
XX
XX New universal primers, mcb 398 and mcb 869, capable of amplifying a
XX fragment of cytochrome b gene of any animal species, useful for
XX establishing the identity of biological materials and animals for
XX molecular evidence in forensics.
XX
XX Example 1; Page 28-57; 128pp; English.
XX
XX The present invention describes universal primers, mcb 398 and mcb 869
XX (see ABQ83297 and ABQ83298), capable of amplifying a fragment of
XX cytochrome b gene of any animal species in polymerase chain reaction
XX (PCR) and revealing the identity of the biological material of any animal
XX of unknown origin at species and sub-species level. Also described is a
XX method for the identification of the animal from a biological sample. The
XX method is used for animal identification to establish the crime with the
XX criminal beyond a reasonable doubt, to establish the identity of
XX biological materials such as skin, horns confiscated from animal
XX poachers, if it is that of an endangered species, for the purpose of
XX molecular evidence of animal hunting and related crime in the court of
XX law, so that human violation of the wildlife resources could be
XX controlled, to have an idea of the geographical location of the
XX poached animal identified by the universal primer invented, to detect the
XX adulteration of animal meat in food products for the purpose of food
XX fortification, by the food fortification agencies, to provide a universal
XX technique for detection of the origin of blood or blood stains collected
XX from the scene of the crime related to offenses such as murder and rape,
XX in order to establish the origin of blood found at the scene of the crime
XX when it sounds as if criminals intentionally spread the blood of an
XX animal at the scene of the crime to confuse the crime investigators and
XX forensic scientists with human blood, and so that the method can be
XX converted to a commercial molecular kit and DNA chips based applications
XX for wildlife identification in forensics. The present sequence represents
XX a mitochondrial cytochrome b gene sequence from the present invention
XX
SQ Sequence 472 BP; 143 A; 153 C; 60 G; 116 T; 0 U; 0 Other;
Query Match 83.1%; Score 392; DB 8; Length 472;
Best Local Similarity 89.4%; Pred. No. 1.9e-112;
Matches 422; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
QY 1 TACCATGAGGACAAATATCTTTTTCAGGAGCAACAGTATCATCAACCAATCTCTTTTCAGCAA 60
DB 1 TCCCATATACCGTACCAACCTAGTAGATGAATCTGAGGAGGTTCTCAGTAGATAAG 120
QY 61 TCCCATATACCGTACCAACCTAGTAGATGAATCTGAGGAGGTTCTCAGTAGATAAG 120
DB 61 TCCCATATATGGTACAAACCTAGTAGATGAATCTGAGGAGGTTCTCAGTAGATAAG 120
QY 121 CAACCTTTACCGGATTTTTCGCTTCCACTTTATCTCTCCATTTATCATTTGAGCCCTTA 180
DB 121 CAACCTTTACCGGATTTTTCGCTTCCACTTTATCTCTCCATTTATCATTTGAGCCCTTA 180
QY 181 CCATAGTACACCTACTGTGTTTCCAGAAACAGGATCCAAACCCCAACAGGAATCTCAT 240
DB 181 CCATAGTACACCTACTGTGTTTCCAGAAACAGGATCCAAACCCCAACAGGAATCTCAT 240
QY 241 CAGACGACAGCAAAATTCATTTCCACCCCTACTACACTATCAAGATATCTTAGAGCTC 300

Db	241	CAGATGCAGATAAAATTCCATTCCACCCCTACTACCATCAAGACATCTAGGCGCC	300
Qy	301	TACTATTAAATTTAACCTCATGCTTCTAGTCTTATTTCCACCGACCTGCTTGGAGACC	360
Db	301	TACTACTAAATTTCTAGCCCTCATATTACTAGTACTATTTCACCCGACCTGCTCGGAGACC	360
Qy	361	CAGACAACTATACACACGACCAACCCACTTAATACACCCCCACATATCAAGCCCGAATGAT	420
Db	361	CAGACGAATACACCCCGACACCCACTTAATACACCCCTCATATCAAAACCCGAATGAT	420
Qy	421	ACTTCTATTGGCATACGCAATTCCTCGATCAATTCCTAACAACTAGGAGG	472
Db	421	ATTTCCTATTGGCATACGCAATTCCTAGATCAATCCCAATAAAGTAGGAGG	472
RESULT 3			
ABQ83307			
ID ABQ83307 standard; DNA; 472 BP.			
XX	ABQ83307;		
XX			
DT	18-JAN-2003 (first entry)		
DE	Mitochondrial cytochrome b gene sequence SEQ ID NO:12.		
KW	Mitochondrial cytochrome b gene; mitochondrial; cytochrome b;		
KW	identification; criminal investigation; animal poaching; gene; ds.		
OS	Unidentified.		
XX	WO200272728-A1.		
XX	03-OCT-2002.		
XX	28-MAR-2001; 2001WO-IN000055.		
XX	28-MAR-2001; 2001WO-IN000055.		
PA	(COUL) COUNCIL SCI & IND RES.		
XX	Verma SK, Singh L;		
XX	WPI; 2003-018945/01		
DR			

CC	animal at the scene of the crime to confuse the crime investigators and
CC	forensic scientists with human blood, and so that the method can be
CC	converted to a commercial molecular kit and DNA chips based applications
CC	for wildlife identification in forensics. The present sequence represents
CC	a mitochondrial cytochrome b gene sequence from the present invention
XX	
SQ	Sequence 472 BP; 141 A; 153 C; 66 G; 112 T; 0 U; 0 Other;
	Query Match 82.0%; Score 387.2; DB 8; Length 472;
	Best Local Similarity 88.8%; Pred. No. 6.1e-111;
	Matches 419; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
QY	1 TACCATGAGACAAAATATCTTTTGGAGGACAACAGTCATCACCAATCTCCTTTTCAGCAA 60
Db	
	1 TGCCATGAGACAAAATATCATCTCGAGGGGCAACAGATCATCACCAATCTCTCTCAGCAA 60
QY	61 TCCCATACATCGGTACAAACTAGTAGAATGAATCTCGAGGAGGTTCCTCAGTAGATAAAG 120
Db	
	61 TCCCATATATTGSCACAGACTAGTAGAATGAATCTGAGGAGGATTATCACTAGACAAG 120
QY	121 CAACCCCTTACCCGATTTTTCGCCTTCCACATTATCTCTCCCAATTATCATTTGCAGGCCCTTA 180
Db	
	121 CAACCCCTTACCCGATTTTTCGCCTTCCACATTATCTCTCCCATTCACTTGCGAGCCCTTG 180
QY	181 CCATAGTAGACCTACTGCTTTTCTCCAGCAAAACAGATCCAACAACCCACAGGAATCTTCAT 240
Db	
	181 CCATAGTTCACTCTTTATTTCCTCCAGAAAACAGGATCTAACAAACCCACAGGAATCTCGT 240
QY	241 CAGACGACAGACAAAATTCCACTTCACCCCTTACTACACTATCAAAAGATATCCTAGGAGCTC 300
Db	
	241 CAGACGAGATATAAATCCCAATTCACCCCTTACTATACAAATCAGGACATTTCTAGGCGCC 300
QY	301 TACTATTAAATTTTAAACCCCTCATGCTTCTAGTCTTATTTCTACCCGACCTGCTTGGAGACC 360
Db	
	301 TATTACTAATTTAGCCCTCATACTACTAGTACTATTTCGACCCGACCTGCTCGGAGACC 360
QY	361 CAGACAACTATACACGAGAAACCCACTTAATACACCCCAATATCAAGCCCGAATCAT 420
Db	
	361 CAGACAACTACACCCCGCGAACCCTTAACACACCCCTTCACATCAAGCCCGAATGAT 420
QY	421 ACTTCTTATTGGATAGCAATCTCCGATCAATTTCTTAACAAACTAGGAGG 472
Db	
	421 ATTTCCTATTGGATACGCAATCTTACGATCAATCCCCCTAACAACTAGGAGG 472
RESULT 4	
ABQ83306	
ID	ABQ83306 standard; DNA; 472 BP.
XX	
XX	ABQ83306;
XX	
DT	18-JAN-2003 (first entry)
XX	
DE	Mitochondrial cytochrome b gene sequence SEQ ID NO:11.
XX	
KW	Mitochondrial cytochrome b gene; mitochondrial; cytochrome b;
KW	identification; criminal investigation; animal poaching; gene; ds.
XX	
OS	Unidentified.
XX	
FN	WO20027278-A1.
XX	
PD	03-OCT-2002.
XX	
PF	28-MAR-2001; 2001WO-IN000055.
XX	
PR	28-MAR-2001; 2001WO-IN000055.
XX	
PA	(COUL) COUNCIL SCI & IND RES.
XX	
PI	Verma SK, Singh L;
DR	WPI; 2003-018945/01.
XX	

XX New universal primers, mcb 398 and mcb 869, capable of amplifying a
PT fragment of cytochrome b gene of any animal species, useful for
PT establishing the identity of biological materials and animals for
PT molecular evidence in forensics.
XX
PS
PS Example 1; Page 28-57; 128pp; English.
XX
XX The present invention describes universal primers, mcb 398 and mcb 869
CC (see ABQ83297 and ABQ83298), capable of amplifying a fragment of
CC cytochrome b gene of any animal species in polymerase chain reaction
CC (PCR) and revealing the identity of the biological material of any animal
CC of unknown origin at species and sub-species level. Also described is a
CC method for the identification of the animal from a biological sample. The
CC method is used for animal identification to establish the crime with the
CC criminal beyond a reasonable doubt, to establish the identity of
CC biological materials such as skin, horns confiscated from animal
CC poachers, if it is that of an endangered species, for the purpose of
CC molecular evidence of animal hunting and related crime in the court of
CC law, so that human violation of the wildlife resources could be
CC controlled, to have an idea of the geographical location of the
CC commitment of wildlife crime based on the cytochrome b gene haplotype of
CC poached animal identified by the universal primer invented, to detect the
CC adulteration of animal meat in food products for the purpose of food
CC fortification, by the food fortification agencies, to provide a universal
CC technique for detection of the origin of blood or blood stains collected
CC from the scene of the crime related to offenses such as murder and rape,
CC in order to establish the origin of blood found at the scene of the crime
CC when it sounds as if criminals intentionally spread the blood of an
CC animal at the scene of the crime to confuse the crime investigators and
CC forensic scientists with human blood, and so that the method can be
CC converted to a commercial molecular kit and DNA chips based applications
CC for wildlife identification in forensics. The present sequence represents
CC a mitochondrial cytochrome b gene sequence from the present invention
XX
SQ Sequence 472 BP; 140 A; 153 C; 66 G; 113 T; 0 U; 0 Other;
Query Match 81.4%; Score 384; DB 8; Length 472;
Best Local Similarity 88.3%; Pred. No. 6.1e-110; Indels 0; Gaps 0;
Matches 417; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
Qy 1 TACCATGAGGACAAATATCTTTTGGAGGACAAAGTCATCACCACATCTCTCTCAGCAA 60
Db 1 TCCCATATATGGCAGACACCTAGTAATGAATCTGAGGGGCAACAGTCATCACCACATCTCTCTCAGCAA 60
Qy 61 TCCCATATATGGCAGACACCTAGTAATGAATCTGAGGGGCAACAGTCATCACCACATCTCTCTCAGCAA 120
Db 61 TCCCATATATGGCAGACACCTAGTAATGAATCTGAGGGGCAACAGTCATCACCACATCTCTCTCAGCAA 120
Qy 121 CAACCCCTTACCCGATTTTTCGCTTCCACTTTATCTCTCCCATTTATCTATTCAGCCCTTA 180
Db 121 CAACCCCTTACCCGATTTTTCGCTTCCACTTTATCTCTCCCATTTATCTATTCAGCCCTTTG 180
Qy 181 CCATAGTACCTACTGTTTCTCCAGAAACAGATCAACATCAAGATATCTAGAGCTC 240
Db 181 CCATAGTACCTACTGTTTCTCCAGAAACAGATCAACATCAAGATATCTAGAGCTC 240
Qy 241 CAGAGCAGACAAATATCCATTCACCCCTACTACTATCAAGATATCTAGAGCTC 300
Db 241 CAGAGCAGATATAATCCCATTCACCCCTACTACTATAAATCAAGATATCTAGAGCTC 300
Qy 301 TACTATTAATTTTAACCCCTCATGCTTCTAGTCTCTTATCTTCTACCCGAGCTGCTGGAGACC 360
Db 301 TATTACTAATCTAGCCCTCATACTACTAGTACTATTTCGACCCGACCTGCTGGAGACC 360
Qy 361 CAGACATATATACACGAGCAACCCACTTATATACACCCCAATATCAAGCCCAATGAT 420
Db 361 CAGACATATACACCCGAGCAACCCACTTATATACACCCCAATATCAAGCCCAATGAT 420
Qy 421 ACTTCCTATTGTGATAGGCAATCTCGGATCAATTTCTTAACAACTAGGAGG 472
Db 421 ATTTCCTATTGTGATAGGCAATCTCGGATCAATTTCTTAACAACTAGGAGG 472

RESULT 5
ABQ83321
ID ABQ83321 standard; DNA; 472 BP.
XX
XX AC ABQ83321;
XX
XX DT 18-JAN-2003 (first entry)
XX
XX DE Mitochondrial cytochrome b gene sequence SEQ ID NO:26.
XX
XX KW Mitochondrial cytochrome b gene; mitochondrial; cytochrome b;
KW identification; criminal investigation; animal poaching; gene; ds.
XX
XX OS Unidentified.
XX
XX PN WO200277278-A1.
XX
XX PD 03-OCT-2002.
XX
XX PF 28-MAR-2001; 2001WO-IN000055.
XX
XX PR 28-MAR-2001; 2001WO-IN000055.
XX
XX PA (COUL) COUNCIL SCI & IND RES.
XX
XX PI Verma SK, Singh L;
XX
XX WPI; 2003-018945/01.
XX
XX New universal primers, mcb 398 and mcb 869, capable of amplifying a
fragment of cytochrome b gene of any animal species, useful for
PT establishing the identity of biological materials and animals for
PT molecular evidence in forensics.
XX
XX Example 1; Page 28-57; 128pp; English.
XX
XX The present invention describes universal primers, mcb 398 and mcb 869
CC (see ABQ83297 and ABQ83298), capable of amplifying a fragment of
CC cytochrome b gene of any animal species in polymerase chain reaction
CC (PCR) and revealing the identity of the biological material of any animal
CC of unknown origin at species and sub-species level. Also described is a
CC method for the identification of the animal from a biological sample. The
CC method is used for animal identification to establish the crime with the
CC criminal beyond a reasonable doubt, to establish the identity of
CC biological materials such as skin, horns confiscated from animal
CC poachers, if it is that of an endangered species, for the purpose of
CC molecular evidence of animal hunting and related crime in the court of
CC law, so that human violation of the wildlife resources could be
CC controlled, to have an idea of the geographical location of the
CC commitment of wildlife crime based on the cytochrome b gene haplotype of
CC poached animal identified by the universal primer invented, to detect the
CC adulteration of animal meat in food products for the purpose of food
CC fortification, by the food fortification agencies, to provide a universal
CC technique for detection of the origin of blood or blood stains collected
CC from the scene of the crime related to offenses such as murder and rape,
CC in order to establish the origin of blood found at the scene of the crime
CC when it sounds as if criminals intentionally spread the blood of an
CC animal at the scene of the crime to confuse the crime investigators and
CC forensic scientists with human blood, and so that the method can be
CC converted to a commercial molecular kit and DNA chips based applications
CC for wildlife identification in forensics. The present sequence represents
CC a mitochondrial cytochrome b gene sequence from the present invention
XX
SQ Sequence 472 BP; 144 A; 154 C; 62 G; 112 T; 0 U; 0 Other;
Query Match 81.4%; Score 384; DB 8; Length 472;
Best Local Similarity 88.3%; Pred. No. 6.1e-110; Indels 0; Gaps 0;
Matches 417; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
Qy 1 TACCATGAGGACAAATATCTTTTGGAGGACAAAGTCATCACCACATCTCTCTCAGCAA 60
Db 1 TACCATGAGGACAAATATCTTTTGGAGGACAAAGTCATCACCACATCTCTCTCAGCAA 60

[illegible]

RESULT 6
ABQ83333
ID ABQ83333 standard; DNA; 472 BP.
XX
XX AC ABQ83333;
XX AC
XX DT 18-JAN-2003 (first entry)
XX
XX Mitochondrial cytochrome b gene sequence SEQ ID NO:38.
DE
DE Mitochondrial cytochrome b gene; mitochondrial; cytochrome b;
XX KW identification; criminal investigation; animal poaching; gene; ds.
XX KW
XX OS Unidentified.
XX OS
XX PN WO200277278-A1.
XX
XX 03-OCT-2002.
XX
XX 28-MAR-2001; 2001WO-IN000055.
XX PF
XX 28-MAR-2001; 2001WO-IN000055.
XX PR
XX (COUL) COUNCIL SCI & IND RES.
XX PA
XX Verma SK, Singh L;
XX PI
XX WPI: 2003-018945/01.
XX DR

PS Example 1; Page 28-57; 129pp; English.

criminal beyond a reasonable doubt, to establish the identity of biological materials such as skin, horns confiscated from animal poachers, if it is that of an endangered species, for the purpose of molecular evidence of animal hunting and related crime in the court of law, so that human violation of the wildlife resources could be controlled, to have an idea of the geographical location of the commitment of wildlife crime based on the cytochrome b gene haplotype of poached animal identified by the universal primer invented, to detect the adulteration of animal meat in food products for the purpose of food fortification, by the food fortification agencies, to provide a universal technique for detection of the origin of blood or blood stains collected from the scene of the crime related to offenses such as murder and rape, in order to establish the origin of blood found at the scene of the crime when it sounds as if criminals intentionally spread the blood of an animal at the scene of the crime to confuse the crime investigators and forensic scientists with human blood, and so that the method can be converted to a commercial molecular kit and DNA chips based applications for wildlife identification in forensics. The present sequence represents a mitochondrial cytochrome b gene sequence from the present invention

Sequence 472 BP: 141 A; 153 C; 60 G; 118 T; 0 U; 0 Other;

Query Match	79.7%	Score 376	DB 8	Length 472
Best Local Similarity	87.3%	Pred. No. 2e-107		
Matches 412	Conservative 0	Mismatches 60	Indels 0	Gaps 0
Qy 1	TACCATGAGGACAAATATCTTTTGTAGGACCAACAGTCATCACCACATCTCTTTTCAGCAA	60		

61	QY	TCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGTTCTCTAGTAGATAAAG	120
61	Db	TCCCATACATTGGTACAAACTAGTCTGAATATCTGAGGAGGCTTTTCAGTAGACAAG	120
121	QY	CAACCCTTACCCGATTTTGGCTTCCACTTTATCTCCCATTTATCATTTGCGAGCCCTTA	180
121	Db	CAACTCTCACCGGATCTTTGCTTTCCACTTTATCTTCCCTTTTATTATTGCGAGCCCTCG	180
181	QY	CGATAGTACACCTACTGTTTCTCCAGAAACAGGATCCAAACACCCCCACAGGATCTCAT	240
181	Db	CCATAGTTCACTTACTCTTCTCCATGAACAGGATCCAAACACCCCCACAGGAGTCTCAT	240
241	QY	CAGACGACAGAAAATTCGATTCACCCCTACTACACTATCAAGATATCTCTAGGAGTCC	300
241	Db	CGGACGACAGAAAATCCCAATTCACCCCTACTACACATTAAGACATCTCTAGGCGCCC	300
301	QY	TACTATTAAATTTTAAACCGCTCATGTTCTTAGTCTCTATTCTCACCGGACCTGTTGAGAGCC	360
301	Db	TACTACTCATCTTAGCCCTTAATCTCTAGTATTATTCTCACCGGACTTACTTGGAGACC	360
361	QY	CAGACAATATACACACGACAAACCCACTTAAATACACCCCCACATATCAAGCCCGAAATGAT	420
361	Db	CAGATAACTACACCCGAGCAACCCACTCAACACACCTCCCCATATTAAACCCGAAATGAT	420
421	QY	ACTTCCTATTGATAGCGAATCTCTCGATCAATCTCTTAACAAACTAGGAGG	472
421	Db	ACTTCTCTATTGATAGCGAATCTCTAGATCAATCTCAAGATTCCTCAAAACAAACTAGGAGG	472

RESULT 7	
ABQ83331	
ID	ABQ83331 standard; DNA; 472 BP.
XX	
AC	ABQ83331;
XX	
DT	18-JAN-2003 (first entry)
XX	
DE	Mitochondrial cytochrome b gene sequence SEQ ID NO:35.
XX	
KW	Mitochondrial cytochrome b gene; mitochondrial; cytochrome b;
KW	identification; Criminal investigation; animal poaching; gene; ds.
XX	
OS	Unidentified.

CC biological materials such as skin, horns confiscated from animal
CC poachers, if it is that of an endangered species, for the purpose of
CC molecular evidence of animal hunting and related crime in the court of
CC law, so that human violation of the wildlife resources could be
CC controlled, to have an idea of the geographical location of the
CC commitment of wildlife crime based on the cytochrome b gene haplotype of
CC poached animal identified by the universal primer invented, to detect the
CC adulteration of animal meat in food products for the purpose of food
CC fortification, by the food fortification agencies, to provide a universal
CC technique for detection of the origin of blood or blood stains collected
CC from the scene of the crime related to offenses such as murder and rape,
CC in order to establish the origin of blood found at the scene of the crime
CC when it sounds as if criminals intentionally spread the blood of an
CC animal at the scene of the crime to confuse the crime investigators and
CC forensic scientists with human blood, and so that the method can be
CC converted to a commercial molecular kit and DNA chips based applications
CC for wildlife identification in forensics. The present sequence represents
CC a mitochondrial cytochrome b gene sequence from the present invention
XX
SQ Sequence 472 BP; 152 A; 140 C; 57 G; 122 T; 0 U; 1 Other;

Query Match 78.8%; Score 371.8; DB 8; Length 472;
Best Local Similarity 86.7%; Pred. No. 4.1e-106;
Matches 409; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 1 TACCATGAGGACAAATATCTTTTGGAGGACACAGTCATCCCATCTCCTTCAGCAA 60
DB 1 TACCATGAGGACAAATATCTTTTGGAGGACACAGTCATCCCATCTCCTTCAGCAA 60
QY 61 TCCCATACATCGGTACAAACCTAGTAGTAGTGAATCTGAGGAGGTTCTCAGTAGATAAAG 120
DB 61 TCCCATACATCGGTACAAACCTAGTAGTAGTGAATCTGAGGAGGTTCTCAGTAGACAAG 120
QY 121 CAACCCCTTACCCGATTTTTCGCTTTCACCTTTATCTCCCATTTATTCATAGCAATTG 180
DB 121 CAACCCCTTACCCGATTTTTCGCTTTCACCTTTATCTCCCATTTATTCATAGCAATTG 180
QY 181 CCATAGTACACCTACTGTTTCTCCAGAACAGGATCCACACCCACAGGAAATCTCAT 240
DB 181 CCATAGTACACCTACTGTTTCTCCAGAACAGGATCCACACCCACAGGAAATTTCTT 240
QY 241 CAGACGACAGACAAATTTCCATTCACCCCTACTACACTATCAAGATATCTTAGGAGCTC 300
DB 241 CAGACGACAGACAAATTTCCATTCACCCCTACTACACTATCAAGATATCTTAGGAGCTC 300
QY 301 TACTATTAAATTTTAAACCTCATGCTTCTAGTCTTATTTCCACGAGCCTGCTTGGAGACC 360
DB 301 TATTACTAATTTCTAACTTAATACTACTAGTACTATTCGACGAGCCTCTCGGAGACC 360
QY 361 CAGACAACTATACACGAGAACCCGCTTAATACACCCCATATACAGCCCGGAATGAT 420
DB 361 CAGATAACTACACCCGAGAAATCCATTAACACACCTCCCCCATCAAAACCCGAATGAT 420
QY 421 ACTTCCTATTTCATAGCAGCAATCTCCGATCAATTTCTTAACAACTAGGAGG 472
DB 421 ACTTCCTATTTCATAGCAATTTTACGGTCAATCCCAACAACTAGGAGG 472

RESULT 12
ABQ83313
ID ABQ83313 standard; DNA; 472 BP.
XX
AC ABQ83313;
XX
DT 18-JAN-2003 (first entry)
XX
DE Mitochondrial cytochrome b gene sequence SEQ ID NO:18.
XX
KW Mitochondrial cytochrome b gene; mitochondrial; cytochrome b;
KW identification; criminal investigation; animal poaching; gene; ds.
XX
OS Unidentified.
XX

PN WO200277278-A1.
XX 03-OCT-2002.
PD 28-MAR-2001; 2001WO-IN0000055.
XX 28-MAR-2001; 2001WO-IN0000055.
XX (COUL) COUNCIL SCI & IND RES.
PA Verma SK, Singh L;
PI WPI; 2003-018945/01.
DR New universal primers, mcb 398 and mcb 869, capable of amplifying a
XX fragment of cytochrome b gene of any animal species, useful for
PT establishing the identity of biological materials and animals for
PT molecular evidence in forensics.
XX
PS Example 1; Page 28-57; 128pp; English.
XX
CC The present invention describes universal primers, mcb 398 and mcb 869
CC (see ABQ83297 and ABQ83298), capable of amplifying a fragment of
CC cytochrome b gene of any animal species in polymerase chain reaction
CC (PCR) and revealing the identity of the biological material of any animal
CC of unknown origin at species and sub-species level. Also described is a
CC method for the identification of the animal from a biological sample. The
CC method is used for animal identification to establish the crime with the
CC criminal beyond a reasonable doubt, to establish the identity of
CC biological materials such as skin, horns confiscated from animal
CC poachers, if it is that of an endangered species, for the purpose of
CC molecular evidence of animal hunting and related crime in the court of
CC law, so that human violation of the wildlife resources could be
CC controlled, to have an idea of the geographical location of the
CC commitment of wildlife crime based on the cytochrome b gene haplotype of
CC poached animal identified by the universal primer invented, to detect the
CC adulteration of animal meat in food products for the purpose of food
CC fortification, by the food fortification agencies, to provide a universal
CC technique for detection of the origin of blood or blood stains collected
CC from the scene of the crime related to offenses such as murder and rape,
CC in order to establish the origin of blood found at the scene of the crime
CC when it sounds as if criminals intentionally spread the blood of an
CC animal at the scene of the crime to confuse the crime investigators and
CC forensic scientists with human blood, and so that the method can be
CC converted to a commercial molecular kit and DNA chips based applications
CC for wildlife identification in forensics. The present sequence represents
CC a mitochondrial cytochrome b gene sequence from the present invention
XX
SQ Sequence 472 BP; 147 A; 145 C; 63 G; 117 T; 0 U; 0 Other;

Query Match 78.6%; Score 371.2; DB 8; Length 472;
Best Local Similarity 86.7%; Pred. No. 6.4e-106;
Matches 409; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 1 TACCATGAGGACAAATATCTTTTGGAGGACACAGTCATCCCATCTCCTTCAGCAA 60
DB 1 TACCATGAGGACAAATATCTTTTGGAGGACACAGTCATCCCATCTCCTTCAGCAA 60
QY 61 TCCCATACATCGGTACAAACCTAGTAGTAGTGAATCTGAGGAGGTTCTCAGTAGATAAAG 120
DB 61 TCCCATACATCGGTACAAACCTAGTAGTAGTGAATCTGAGGAGGTTCTCAGTAGACAAG 120
QY 121 CAACCCCTTACCCGATTTTTCGCTTTCACCTTTATCTCCCATTTATTCATTCAGCCCTTA 180
DB 121 CAACCCCTTACCCGATTTTTCGCTTTCACCTTTATCTCCCATTTATTCATTCAGCCCTCG 180
QY 181 CCATAGTACACCTACTGTTTCTCCAGGAAACAGGATCCCAACCCACAGGAAATCTCAT 240
DB 181 CAATATCCATCTACTCTTCTCCATGAACAGGCTCAACATCCCAACAGGAAATTCAT 240
QY 241 CAGACGACAGACAAATTTCCATTCACCCCTACTACACTATCAAGATATCTTAGGAGCTC 300
DB 241 CAGACGACAGATAAATCCCATTTTCCACCCCTACTACACTATTAAGACATTTCTAGGAGCCC 300

PT fragment of cytochrome b gene of any animal species, useful for
PT establishing the identity of biological materials and animals for
XX molecular evidence in forensics.

XX Example 1; Page 28-57; 128pp; English.

XX The present invention describes universal primers, mcb 398 and mcb 869
CC (see ABQ83297 and ABQ83298), capable of amplifying a fragment of
CC cytochrome b gene of any animal species in polymerase chain reaction
CC (PCR) and revealing the identity of the biological material of any animal
CC of unknown origin at species and sub-species level. Also described is a
CC method for the identification of the animal from a biological sample. The
CC method is used for animal identification to establish the crime with the
CC criminal beyond a reasonable doubt, to establish the identity of
CC biological materials such as skin, horns confiscated from animal
CC poachers, if it is that of an endangered species, for the purpose of
CC molecular evidence of animal hunting and related crime in the court of
CC law, so that human violation of the wildlife resources could be
CC controlled, to have an idea of the geographical location of the
CC commitment of wildlife crime based on the cytochrome b gene haplotype of
CC poached animal identified by the universal primer invented, to detect the
CC adulteration of animal meat in food products for the purpose of food
CC fortification, by the food fortification agencies, to provide a universal
CC technique for detection of the origin of blood or blood stains collected
CC from the scene of the crime related to offenses such as murder and rape,
CC in order to establish the origin of blood found at the scene of the crime
CC when it sounds as if criminals intentionally spread the blood of an
CC animal at the scene of the crime to confuse the crime investigators and
CC forensic scientists with human blood, and so that the method can be
CC converted to a commercial molecular kit and DNA chips based applications
CC for wildlife identification in forensics. The present sequence represents
CC a mitochondrial cytochrome b gene sequence from the present invention
XX

SQ Sequence 472 BP; 143 A; 157 C; 59 G; 113 T; 0 U; 0 Other;

Query Match 78.6%; Score 371.2; DB 8; Length 472;
Best Local Similarity 86.7%; Pred. No. 6.4e-106;
Matches 409; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 1 TACCATTGAGGACAAATATCTTTTGGAGGACCAACAGTCATCACCAATCTCTTTCAGCAA 60
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DB 121 CCACCCCTGACCCGATTTTTCGCTTTCACCTTTATTTCCCATTCATCGCAGCCCTCG 180
QY 181 CCATGATACCTACTCTGTTTCTCGAAGACAGGATCCACACCCACAGGATCTCAT 240
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DB 241 CGGACACAGATAAATTCCTTCCACCCCTTACTACACCATTAAGACATCTAGTGCCA 300
QY 301 TACTATTAAATTTAAACCTCATGCTTCTAGTCCCTATTCTCACCGGACCTGCTTGAGACC 360
DB 301 TCCTACTAATCTCACTCATCTACTAGTACTATTACGCGCTGACCTACTCGGAGACC 360
QY 361 CAGACAACTATACACGAGAAACCCATTATATACACCCCAATATCAAGCCCAATGAT 420
DB 361 CAGACAACTATACACCCGAGAAACCCATTATATACACCCCAATATCAAGCCCAATGAT 420
QY 421 ACTTCCTATTGGATAGCAATCTCGATCAATTTCTTACCACTAGGAGG 472
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RESULT 15

ABQ83310
ID ABQ83310 standard; DNA; 472 BP.

XX AC ABQ83310;

XX DT 18-JAN-2003 (first entry)

XX DE Mitochondrial cytochrome b gene sequence SEQ ID NO:15.

XX KW Mitochondrial cytochrome b gene; mitochondrial; cytochrome b;
XX identification; criminal investigation; animal poaching; gene; ds.

XX OS Unidentified.

XX PN WO200277278-A1.

XX PD 03-OCT-2002.

XX PF 28-MAR-2001; 2001WO-IN000055.

XX PR 28-MAR-2001; 2001WO-IN000055.

XX PA (COUL) COUNCIL SCI & IND RES.

XX PI Verma SK, Singh L;

XX DR WPI; 2003-018945/01.

XX New universal primers, mcb 398 and mcb 869, capable of amplifying a
PT fragment of cytochrome b gene of any animal species, useful for
PT establishing the identity of biological materials and animals for
PT molecular evidence in forensics.

XX Example 1; Page 28-57; 128pp; English.

XX The present invention describes universal primers, mcb 398 and mcb 869
CC (see ABQ83297 and ABQ83298), capable of amplifying a fragment of
CC cytochrome b gene of any animal species in polymerase chain reaction
CC (PCR) and revealing the identity of the biological material of any animal
CC of unknown origin at species and sub-species level. Also described is a
CC method for the identification of the animal from a biological sample. The
CC method is used for animal identification to establish the crime with the
CC criminal beyond a reasonable doubt, to establish the identity of
CC biological materials such as skin, horns confiscated from animal
CC poachers, if it is that of an endangered species, for the purpose of
CC molecular evidence of animal hunting and related crime in the court of
CC law, so that human violation of the wildlife resources could be
CC controlled, to have an idea of the geographical location of the
CC commitment of wildlife crime based on the cytochrome b gene haplotype of
CC poached animal identified by the universal primer invented, to detect the
CC adulteration of animal meat in food products for the purpose of food
CC fortification, by the food fortification agencies, to provide a universal
CC technique for detection of the origin of blood or blood stains collected
CC from the scene of the crime related to offenses such as murder and rape,
CC in order to establish the origin of blood found at the scene of the crime
CC when it sounds as if criminals intentionally spread the blood of an
CC animal at the scene of the crime to confuse the crime investigators and
CC forensic scientists with human blood, and so that the method can be
CC converted to a commercial molecular kit and DNA chips based applications
CC for wildlife identification in forensics. The present sequence represents
CC a mitochondrial cytochrome b gene sequence from the present invention
XX

SQ Sequence 472 BP; 139 A; 157 C; 61 G; 115 T; 0 U; 0 Other;

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Matches 408; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

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QY 61 TCCCATACATCGGTACAAACCTAGTAGAATCTGAGGAGGTTCTCAGTAGATAAG 120

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: November 16, 2004, 22:33:39 ; Search time 142.229 Seconds
(without alignments)
8644.709 Million cell updates/sec

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Perfect score: 26
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 4526729 seqs, 23644849745 residues
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Minimum DB seq length: 0
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Listing first 45 summaries

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2: gb.htg:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	26	100.0	26	6	AX565562	AX565562 Sequence
C 2	26	100.0	327	5	AF123633	AF123633 Perissoco
C 3	26	100.0	375	5	AF123617	AF123617 Pipreola
C 4	26	100.0	378	5	AF127194	AF127194 Gallaria
C 5	26	100.0	378	5	AF127202	AF127202 Hylopezus
C 6	26	100.0	472	6	AX565570	AX565570 Sequence
C 7	26	100.0	472	6	AX565571	AX565571 Sequence
C 8	26	100.0	477	5	AF376882	AF376882 Yuhina za
C 9	26	100.0	892	5	CFU81343	U91343 Chelus fimb
C 10	26	100.0	912	5	AY150649	AY150649 Androdon
C 11	26	100.0	929	10	U86834	U86834 Phyllotis w
C 12	26	100.0	999	5	AY065699	AY065699 Lochmias
C 13	26	100.0	999	5	AY065721	AY065721 Hylopezus
C 14	26	100.0	1056	3	AF189111	AF189111 Cryptoter
C 15	26	100.0	1111	5	AY188015	AY188015 Dromicodr
C 16	26	100.0	1117	5	AF217828	AF217828 Aspidelap
C 17	26	100.0	1125	5	AF009931	AF009931 Archocent
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C 28	26	100.0	1140	4	AB122100	AB122100 Tragulus
C 29	26	100.0	1140	4	AB122101	AB122101 Tragulus
C 30	26	100.0	1140	4	AB122102	AB122102 Tragulus
C 31	26	100.0	1140	4	AB122103	AB122103 Tragulus
C 32	26	100.0	1140	4	AB122104	AB122104 Tragulus
C 33	26	100.0	1140	4	AB122105	AB122105 Tragulus
C 34	26	100.0	1140	4	AB122110	AB122110 Tragulus
C 35	26	100.0	1140	4	AF034967	AF034967 Sigmocero
C 36	26	100.0	1140	4	D82890	D82890 Bubalus dep
C 37	26	100.0	1140	4	D88639	D88639 Bubalus dep
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ALIGNMENTS

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LOCUS AX565562
DEFINITION Sequence 3 from Patent WO02077278.
ACCESSION AX565562
VERSION AX565562.1 GI:26000912
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Verma,S.K. and Singh,I.
TITLE Universal primers for wildlife identification
JOURNAL Patent: WO 02077278-A 3 03-OCT-2002;
Council of Scientific and Industrial Research (IN)
LOCATION/Qualifiers
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Db 1 CCTCCTAGTTTGTAGGGATTGATCG 26
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RESULT 2
LOCUS AF123633/c
DEFINITION Perissococephalus tricolor cytochrome b gene, partial cds;
mitochondrial gene for mitochondrial product.
ACCESSION AF123633
VERSION AF123633.1 GI:8050379
KEYWORDS

```

SOURCE      mitochondrion Perissocephalus tricolor (capuchinbird)
ORGANISM    Perissocephalus tricolor
REFERENCE   1  (bases 1 to 327)
AUTHORS     Prum,R.O., Rice,N.H., Mobley,J.A. and Dimmick,W.W.
TITLE       A Preliminary Phylogenetic Hypothesis for the Cotingas (Cotingidae)
JOURNAL     Auk 117 (1), 236-241 (2000)
REFERENCE   2  (bases 1 to 327)
AUTHORS     Prum,R.O., Rice,N.H., Mobley,J.A. and Dimmick,W.W.
TITLE       Direct Submission
JOURNAL     Submitted (26-JAN-1999) Systematics and Ecology, University of
            Kansas, Natural History Museum, Lawrence, KS 66045, USA
FEATURES   Location/Qualifiers
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LOCUS      AF123617             375 bp DNA linear VRT 01-MAY-2002
DEFINITION Pipreola arcuata cytochrome b gene, partial cds; mitochondrial gene
            for mitochondrial product.
ACCESSION  AF123617
VERSION    AF123617.1 GI:8050348
KEYWORDS   .
SOURCE     .
ORGANISM   mitochondrion Pipreola arcuata (barred fruiteater)
            Pipreola arcuata
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Passeriformes; Cotingidae; Pipreola.
REFERENCE   1  (bases 1 to 375)
AUTHORS     Prum,R.O., Rice,N.H., Mobley,J.A. and Dimmick,W.W.
TITLE       A Preliminary Phylogenetic Hypothesis for the Cotingas (Cotingidae)
JOURNAL     Auk 117 (1), 236-241 (2000)
REFERENCE   2  (bases 1 to 375)
AUTHORS     Prum,R.O., Rice,N.H., Mobley,J.A. and Dimmick,W.W.
TITLE       Direct Submission
JOURNAL     Submitted (26-JAN-1999) Systematics and Ecology, University of
            Kansas, Natural History Museum, Lawrence, KS 66045, USA
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RESULT 4
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LOCUS      AF127194             378 bp DNA linear VRT 08-MAY-2000
DEFINITION Grallaria guatemalensis cytochrome b gene, partial cds;
            mitochondrial gene for mitochondrial product.
ACCESSION  AF127194
VERSION    AF127194.1 GI:7715712
KEYWORDS   .
SOURCE     .
ORGANISM   mitochondrion Grallaria guatemalensis (scaled antpitta)
            Grallaria guatemalensis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Passeriformes; Formicariidae;
            Grallaria.
REFERENCE   1  (bases 1 to 378)
AUTHORS     Krabbe,N., Agro,D.J., Rice,N.H., Jacome,M., Navarrete,L. and
            Sornoza,M.F.
TITLE       A new species of antpitta (Formicariidae: Grallaria) from the
            southern Ecuadorian Andes
JOURNAL     Auk 116 (4), 882-890 (1999)
REFERENCE   2  (bases 1 to 378)
AUTHORS     Krabbe,N., Agro,D.J., Rice,N.H., Jacome,M., Navarrete,L. and
            Sornoza,M.F.
TITLE       Direct Submission
JOURNAL     Submitted (10-FEB-1999) Ecology and Evolutionary Biology,
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            USA
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Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 107 CCTCTAGTTTGTAGGATTCG 82

RESULT 5
AF127202/c
LOCUS      AF127202             378 bp DNA linear VRT 08-MAY-2000
DEFINITION Hylopezus fulviventris cytochrome b gene, partial cds;

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mitochondrial gene for mitochondrial product.

ACCESSION AF127202
 VERSION AF127202.1 GI:7715727
 KEYWORDS
 SOURCE
 ORGANISM
 Hylopezus fulviventrtris (fulvous-bellied antpitta)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Passeriformes; Formicariidae;
 Hylopezus.
 REFERENCE 1 (bases 1 to 378)
 AUTHORS Krabbe,N., Agro,D.J., Rice,N.H., Jacome,M., Navarrete,L. and Sornoz,M.F.
 TITLE A new species of antpitta (Formicariidae: Grallaria) from the southern Ecuadorian Andes
 JOURNAL Auk 116 (4):882-890 (1999)
 REFERENCE 2 (bases 1 to 378)
 AUTHORS Krabbe,N., Agro,D.J., Rice,N.H., Jacome,M., Navarrete,L. and Sornoz,M.F.
 TITLE Direct Submission
 JOURNAL Submitted (10-FEB-1999) Ecology and Evolutionary Biology, University of Kansas, Natural History Museum, Lawrence, KS 66045, USA

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 DEFINITION Sequence 11 from Patent WO02077278.
 ACCESSION AX565570
 VERSION AX565570.1 GI:26000920
 KEYWORDS
 SOURCE
 ORGANISM
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Alcelaphinae; Alcelaphus.

REFERENCE 1
 AUTHORS Verma,S.K. and Singh,L.
 TITLE Universal primers for wildlife identification
 JOURNAL Patent: WO 02077278-A 11 03-OCT-2002;
 Council of Scientific and Industrial Research (IN)
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RESULT 7
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 LOCUS
 DEFINITION Sequence 12 from Patent WO02077278.
 ACCESSION AX565571
 VERSION AX565571.1 GI:26000921
 KEYWORDS
 SOURCE
 ORGANISM
 Sigmoceros lichtensteinii (Lichtenstein's hartebeest)
 Sigmoceros lichtensteinii
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Alcelaphinae; Sigmoceros.

REFERENCE 1
 AUTHORS Verma,S.K. and Singh,L.
 TITLE Universal primers for wildlife identification
 JOURNAL Patent: WO 02077278-A 12 03-OCT-2002;
 Council of Scientific and Industrial Research (IN)
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RESULT 8
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 DEFINITION Yuhina zantholeuca cytochrome b gene, partial cds; mitochondrial gene for mitochondrial product.
 ACCESSION AF376882
 VERSION AF376882.1 GI:21309969
 KEYWORDS
 SOURCE
 ORGANISM
 Yuhina zantholeuca
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Passeriformes; Corvoidea; Corvidae;
 Yuhina.

REFERENCE 1 (bases 1 to 477)
 AUTHORS Cibois,A., Kalyakin,M.V., Han,L.-X. and Pasquet,E.
 TITLE Molecular phylogenetics of babblers (Timaliidae): reevaluation of the genera Yuhina and Stachyris
 JOURNAL J. Avian Biol. 33 (4), 380-390 (2002)
 REFERENCE 2 (bases 1 to 477)
 AUTHORS Cibois,A., Kalyakin,M., Han,L.-X. and Pasquet,E.
 TITLE Direct Submission
 JOURNAL Submitted (07-MAY-2001) Ornithology, Museum National d'Histoire Naturelle, 55 rue Buffon, Paris 75005, France
 REFERENCE 3 (bases 1 to 477)
 AUTHORS Cibois,A., Kalyakin,M., Han,L.-X. and Pasquet,E.
 TITLE Direct Submission
 JOURNAL Submitted (20-JUN-2002) Ornithology, Museum National d'Histoire Naturelle, 55 rue Buffon, Paris 75005, France

REMARK
 Sequence update by submitter
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Db 353 CCTCTAGTTGTTAGGATGATCG 328
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RESULT 9
CFU81343/c
LOCUS
DEFINITION Chelus fimbriata cytochrome b gene, mitochondrial gene encoding
mitochondrial protein, partial cds.
ACCESSION U81343
VERSION U81343.1 GI:2098650
KEYWORDS
SOURCE
ORGANISM
mitochondrion Chelus fimbriatus
Chelus fimbriatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Testudines; Pleurodira; Chelidae; Chelus.
REFERENCE
1 (bases 1 to 892)
Shaffer,H.B., Meylan,P. and McKnight,M.L.
TITLE Tests of turtle phylogeny: molecular, morphological, and
paleontological approaches
JOURNAL Syst. Biol. 46 (2), 235-268 (1997)
MEDLINE 21971902
PUBMED 11975342
REFERENCE
2 (bases 1 to 892)
Shaffer,H.B., Meylan,P. and McKnight,M.L.
DIRECT SUBMISSION
AUTHORS
TITLE
JOURNAL
SUBMITTED (09-DEC-1996) Evolution & Ecology, University of
California, Davis, CA 95616, USA
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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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791 CCTCTAGTTGTTAGGATGATCG 766
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DEFINITION Andronon aequatorialis cytochrome b gene, partial cds;
mitochondrial gene for mitochondrial product.
ACCESSION AY150649
VERSION AY150649.1 GI:37195387
KEYWORDS
SOURCE
ORGANISM
mitochondrion Andronon aequatorialis (tooth-billed hummingbird)
Andronon aequatorialis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Trochiliformes; Trochilidae;
Andronon.
1 (bases 1 to 912)
Bleiwiss,R., Hendrickson,S.L., Berres,M.E., Willis,Y.O. and
Willis,E.O.
TITLE Affinities of the saw-billed hermit (Ramphodon naevius) determined
by cytochrome-b sequence data
JOURNAL Wilson Bull. (2003) In press
REFERENCE
2 (bases 1 to 912)
Bleiwiss,R., Hendrickson,S.L., Berres,M.E., Willis,Y.O. and
Willis,E.O.
DIRECT SUBMISSION
TITLE
JOURNAL
SUBMITTED (16-SEP-2002) Department of Zoology and the Zoological
Museum, University of Wisconsin, 250 North Mills Street, Madison,
WI 53706, USA
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RESULT 11
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LOCUS
DEFINITION Phyllotis wolffsohni MSB 67270 cytochrome b (cytb) gene,
mitochondrial gene encoding mitochondrial protein, partial cds.
ACCESSION U86834
VERSION U86834.1 GI:4218914
KEYWORDS
SOURCE
ORGANISM
mitochondrion Phyllotis wolffsohni (Wolffsohn's leaf-eared mouse)
Phyllotis wolffsohni
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
Phyllotis.
1 (bases 1 to 929)
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AUTHORS Steppan,S.J.
 TITLE Phylogenetic relationships and species limits within Phyllostis (Rodentia: Sigmodontinae): concordance between mtDNA sequence and morphology
 JOURNAL J. Mammal., 79 (2), 573-593 (1998) ,
 REFERENCE 2 (bases 1 to 929)
 AUTHORS Steppan,S.J.
 TITLE Direct Submission
 JOURNAL Submitted (24-JAN-1997) Laboratory of Molecular Systematics, Smithsonian Institution, Museum Support Center, 4210 Silver Hill Road, Suitland, MD 20746, USA
 FEATURES Location/Qualifiers
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 DEFINITION mitochondrial gene for mitochondrial product.
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 VERSION AY065699.1 GI:21805434
 KEYWORDS
 SOURCE mitochondrion Lochimias nematura
 ORGANISM Lochimias nematura
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Passeriformes; Furnariidae; Lochimias.
 REFERENCE 1 (bases 1 to 999)
 AUTHORS Irestedt,M., Fjeldsa,J., Johansson,U.S. and Ericson,P.G.P.
 TITLE Systematic relationships and biogeography of the tracheophone suboscines (Aves: Passeriformes)
 JOURNAL Mol. Phylogenet. Evol. 23 (3), 499-512 (2002)
 MEDLINE PUBMED 1209801
 REFERENCE 2 (bases 1 to 999)
 AUTHORS Irestedt,M., Fjeldsa,J., Johansson,U.S. and Ericson,P.G.P.
 TITLE Direct Submission
 JOURNAL Submitted (05-DEC-2001) Dept. of Vertebrate Zoology, Swedish Museum of Natural History, P.O. Box 50007, Stockholm SE-10405, Sweden
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 DEFINITION mitochondrial gene for mitochondrial product.
 ACCESSION AY065721
 VERSION AY065721.1 GI:21805478
 KEYWORDS
 SOURCE mitochondrion Hylopezus fulviventris (fulvous-bellied antpitta)
 ORGANISM Hylopezus fulviventris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Passeriformes; Formicariidae; Hylopezus.
 REFERENCE 1 (bases 1 to 999)
 AUTHORS Irestedt,M., Fjeldsa,J., Johansson,U.S. and Ericson,P.G.P.
 TITLE Systematic relationships and biogeography of the tracheophone suboscines (Aves: Passeriformes)
 JOURNAL Mol. Phylogenet. Evol. 23 (3), 499-512 (2002)
 MEDLINE PUBMED 1209801
 REFERENCE 2 (bases 1 to 999)
 AUTHORS Irestedt,M., Fjeldsa,J., Johansson,U.S. and Ericson,P.G.P.
 TITLE Direct Submission
 JOURNAL Submitted (05-DEC-2001) Dept. of Vertebrate Zoology, Swedish Museum of Natural History, P.O. Box 50007, Stockholm SE-10405, Sweden
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ACCESSION AF189111
KEYWORDS
SOURCE AF189111.1 GI:10441542
mitochondrion Cryptotermes austrinus

CRYPTOTERMES AUSTRINUS
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Orthopteroidea; Dictyoptera; Isoptera; Kalotermitidae;
Cryptotermitinae; Cryptotermes.
1 (bases 1 to 1056)
Thompson,G.J., Miller,L.R., Lenz,M. and Crozier,R.H.
Phylogenetic analysis and trait evolution in Australian lineages of
drywood termites (Isoptera, Kalotermitidae)
Mol. Phylogenet. Evol. 17 (3), 419-429 (2000)

JOURNAL
MEDLINE
PUBMED
20575775
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REFERENCE
2 (bases 1 to 1056)
Thompson,G.J. and Crozier,R.H.
Direct Submission
Submitted (22-SEP-1999) Genetics & Evolution, La Trobe University,
Kingsbury Drive, Melbourne, VIC 3083, Australia
JOURNAL
FEATURES
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Db 797 CCTCCTAGTTGTTAGGATTGATCG 772

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ACCESSION AF189111
KEYWORDS
SOURCE AF189111.1 GI:37778272
mitochondrion Dromicodryas quadrilineatus

DROMICODRYAS QUADRILINEATUS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Colubridae; Boodontinae; Dromicodryas.
1 (bases 1 to 1111)
Nagy,Z.T., Joger,U., Wink,M., Glaw,F. and Vences,M.
Multiple colonization of Madagascar and Socotra by colubrid snakes:
evidence from nuclear and mitochondrial gene phylogenies
Proc. R. Soc. Lond., B, Biol. Sci. 270, 2613-2621 (2003)
2 (bases 1 to 1111)
Nagy,Z.T., Joger,U., Wink,M., Glaw,F. and Vences,M.
Direct Submission
Submitted (25-NOV-2002) Department of Pharmacy and Molecular
Biotechnology, Biological Section, University of Heidelberg, Im
Neuenheimer Feld 364, Heidelberg 69120, Germany
3 (bases 1 to 1111)
Nagy,Z.T., Joger,U., Wink,M., Glaw,F. and Vences,M.
Direct Submission
Submitted (27-OCT-2003) Department of Pharmacy and Molecular
Biotechnology, Biological Section, University of Heidelberg, Im
Neuenheimer Feld 364, Heidelberg 69120, Germany
Sequence update by submitter
JOURNAL
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Job time : 145.229 secs

AF188015/c

LOCUS
DEFINITION

ACCESSION
KEYWORDS
SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REMARK

FEATURES

source

gene

CDS

QY

Db

Search completed: November 17, 2004, 02:58:40
Job time : 145.229 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 23:55:00 ; Search time 167.862 Seconds
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	286.4	60.7	16568	4	US-09-525-906-1 Sequence 1, Appli
2	286.4	60.7	16569	3	US-09-097-889-2 Sequence 2, Appli
3	286.4	60.7	16569	3	US-09-377-856-1 Sequence 1, Appli
4	286.4	60.7	16569	4	US-09-302-681-2 Sequence 2, Appli
5	286.4	60.7	16569	4	US-09-098-079-2 Sequence 1, Appli
6	286.4	60.7	16569	4	US-10-053-611-1 Sequence 7, Appli
7	284.8	60.3	11440	4	US-09-377-497-7 Sequence 1, Appli
8	195	41.3	614	3	US-09-385-982-185 Sequence 185, App
9	182	38.6	591	3	US-09-385-982-493 Sequence 493, App
10	179.6	38.1	602	3	US-09-385-982-375 Sequence 375, App
11	149.4	31.7	619	3	US-09-385-982-510 Sequence 510, App
12	146	30.6	578	3	US-09-328-111-763 Sequence 763, App
13	130.4	27.6	597	3	US-09-328-111-562 Sequence 562, App
14	127.8	27.1	650	3	US-08-998-416-190 Sequence 190, App
15	127.8	27.1	716	3	US-08-998-416-1032 Sequence 1032, Ap
16	127.8	27.1	835	3	US-08-998-416-533 Sequence 533, App
17	127.8	27.1	836	3	US-08-998-416-286 Sequence 286, App
18	126.4	26.8	668	3	US-09-328-111-812 Sequence 812, App
19	101.4	21.5	255	4	US-09-702-705-719 Sequence 719, App
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26	79.4	16.8	315	4	US-09-313-294A-7516 Sequence 7516, Ap
27	64.6	13.7	759	4	US-09-270-767-11513 Sequence 11513, A

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31	54.6	11.6	1512	4	US-09-252-991A-7793	Sequence 7793, Ap
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36	35.6	7.5	3451	2	US-08-743-637B-18	Sequence 18, Appl
37	35.6	7.5	3451	3	US-08-526-840B-18	Sequence 18, Appl
38	33.4	7.1	840	3	US-09-453-702B-207	Sequence 207, Appl
39	33.2	7.0	505	4	US-09-621-976-15639	Sequence 15639, A
40	32.8	6.9	289	3	US-09-007-005-17	Sequence 17, Appl
41	32.8	6.9	289	3	US-09-244-796-17	Sequence 17, Appl
42	32.8	6.9	2429	3	US-09-386-493-3	Sequence 3, Appli
43	32.6	6.9	832	4	US-09-621-976-2813	Sequence 2813, Ap
44	32.4	6.9	957	4	US-09-248-796A-2649	Sequence 2649, Ap
45	32	6.8	2699	4	US-10-148-689-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-525-906-1
; Sequence 1, Application US/09525906
; Patent No. 6605433
; GENERAL INFORMATION:
; APPLICANT: Jen, Jen
; APPLICANT: Sidransky, David
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; APPLICANT: Fliss, Makiko
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: Mitochondrial Dosimeter
; FILE REFERENCE: 1107.85815
; CURRENT APPLICATION NUMBER: US/09/525,906
; CURRENT FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 09/377,856
; PRIOR FILING DATE: 1999-08-20
; PRIOR APPLICATION NUMBER: 60/097,307
; PRIOR FILING DATE: 1998-08-20
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-525-906-1

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Db 15564 ATTTCCTATTGCTTACACAAATCTCCGATCGTCCCTAACAACTAGGAGG 15615

RESULT 4
US-09-302-681-2
; Sequence 2, Application US/09302681
; Patent No. 6441149
; GENERAL INFORMATION:
; APPLICANT: Hermsstadt, Corrina
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Clevenger, William
; APPLICANT: Fahy, Eoin F.
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: DIAGNOSTIC METHOD OF EXTRAMITOCHONDRIAL DNA
; FILE REFERENCE: 660088.416C1
; CURRENT APPLICATION NUMBER: US/09/302,681
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 16569
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-302-681-2

Query Match 60.7%; Score 286.4; DB 4; Length 16569;
Best Local Similarity 75.4%; Pred. No. 5.3e-86;
Matches 356; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCTTTTGGAGGACAAACAGTCATCAACCAATCTCTTTACGCAA 60
Db 15144 TCCCGTGAGGCCAAATATCATCTTGAGGGGCCACAGTAATACAACTTACTATCCGCCA 15203
QY 61 TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTCTCAGTAGATAAG 120
Db 15204 TCCCATACATTTGGACAGACCTAGTTCAATGAATCTGAGGAGGCTACTCAGTAGACAGTC 15263
QY 121 CAACCTTACCCGATTTTTCGCTTCCACCTTTATCTCCCAATTAATCAATTCGAGCCCTTA 180
Db 15264 CCACCTTCACAGAAATCTTTACCTTTTACCTTTTCACTTCACTTTGCCCCCTTCAATTTGAGCCCTAG 15323
QY 181 CCATAGTACACCTACTGTTTCTCCAGAAACAGGATCCAAACCCACAGGAATCTCAT 240
Db 15324 CAACCTCCACCTCTTATTTGCAAGAACGGGATCAACACCCCTAGGATCACCT 15383
QY 241 CAGACGACAGCAAAATTCACCTCCACCTTACACTATCAAGATATCCTAGGAGCTC 300
Db 15384 CCCATTCCGATAAAATCACCTTCCACCTTACTACAAATCAAAGAGCCCTCGGCTTAC 15443
QY 301 TACTATTAATTTAAACCTCATGCTTCTAGTCTTATCTCAGCGGACCTCTTGGAGACC 360
Db 15444 TTCTCTTCTCTCTCTCTTAATGACATTAACACTATTTCTCACCAGACCTCTTAGGCGACC 15503
QY 361 CAGACAACTATACACGACAAACCCACTTAATACACCCCCACATATCAAGCCCGAATGAT 420
Db 15504 CAGACAAATTAATCCCTAGCCAAACCCCTTAACACCCCTCCACATCAAGCCCGAATGAT 15563
QY 421 ACTTCCTATTGTCATAGCAATCTCCGATCAATTTCTTAACAACTAGGAGG 472
Db 15564 ATTTCCTATTGCTTACACAAATCTCCGATCGTCCCTAACAACTAGGAGG 15615

RESULT 5
US-09-098-079-2
; Sequence 2, Application US/09098079
; Patent No. 6489095
; GENERAL INFORMATION:

; APPLICANT: Hermsstadt, Corrina
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Clevenger, William
; APPLICANT: Fahy, Eoin F.
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: DIAGNOSTIC METHOD BASED ON QUANTIFICATION OF
; TITLE OF INVENTION: EXTRAMITOCHONDRIAL DNA
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/098,079
; FILING DATE: 15-JUN-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rosenman Ph.D., Stephen J.
; REGISTRATION NUMBER: 43,058
; REFERENCE/DOCKET NUMBER: 660088.416
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16569 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-098-079-2

Query Match 60.7%; Score 286.4; DB 4; Length 16569;
Best Local Similarity 75.4%; Pred. No. 5.3e-86;
Matches 356; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCTTTTGGAGGACAAACAGTCATCAACCAATCTCTTTACGCAA 60
Db 15144 TCCCGTGAGGCCAAATATCATCTTGAGGGGCCACAGTAATACAACTTACTATCCGCCA 15203
QY 61 TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTCTCAGTAGATAAG 120
Db 15204 TCCCATACATTTGGACAGACCTAGTTCAATGAATCTGAGGAGGCTACTCAGTAGACAGTC 15263
QY 121 CAACCTTACCCGATTTTTCGCTTCCACCTTTATCTCCCAATTAATCAATTCGAGCCCTTA 180
Db 15264 CCACCTTCACAGAAATCTTTACCTTTTACCTTTTCACTTCACTTTGCCCCCTTCAATTTGAGCCCTAG 15323
QY 181 CCATAGTACACCTACTGTTTCTCCAGAAACAGGATCCAAACCCACAGGAATCTCAT 240
Db 15324 CAACCTCCACCTCTTATTTGCAAGAACGGGATCAACACCCCTAGGATCACCT 15383
QY 241 CAGACGACAGCAAAATTCACCTCCACCTTACACTATCAAGATATCCTAGGAGCTC 300
Db 15384 CCCATTCCGATAAAATCACCTTCCACCTTACTACAAATCAAAGAGCCCTCGGCTTAC 15443
QY 301 TACTATTAATTTAAACCTCATGCTTCTAGTCTTATCTCAGCGGACCTCTTGGAGACC 360
Db 15444 TTCTCTTCTCTCTCTCTTAATGACATTAACACTATTTCTCACCAGACCTCTTAGGCGACC 15503
QY 361 CAGACAACTATACACGACAAACCCACTTAATACACCCCCACATATCAAGCCCGAATGAT 420
Db 15504 CAGACAAATTAATCCCTAGCCAAACCCCTTAACACCCCTCCACATCAAGCCCGAATGAT 15563
QY 421 ACTTCCTATTGTCATAGCAATCTCCGATCAATTTCTTAACAACTAGGAGG 472

Db 15564 ATTTCCTATTGCGCTACACAAATTCCTCGATCGCTCCCTTAACAAACTAGGAGG 15615

RESULT 6

US-10-053-611-1

; Sequence 1, Application US/10053611

; Patent No. 6750021

; GENERAL INFORMATION:

; APPLICANT: Polyvak, Kornelia

; APPLICANT: Vogelstein, Bert

; APPLICANT: Kinzler, Kenneth

; TITLE OF INVENTION: Subtle Mitochondrial Mutations as Tumor

; TITLE OF INVENTION: Markers

; FILE REFERENCE: 1107.82346

; CURRENT APPLICATION NUMBER: US/10/053,611

; CURRENT FILING DATE: 2002-01-24

; PRIOR APPLICATION NUMBER: US/09/377,856

; PRIOR FILING DATE: 1999-08-20

; PRIOR APPLICATION NUMBER: 60/097,307

; PRIOR FILING DATE: 1998-08-20

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 1

; LENGTH: 16569

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-053-611-1

Query Match 60.7%; Score 286.4; DB 4; Length 16569;

Best Local Similarity 75.4%; Pred. No. 5.3e-86;

Matches 356; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

Qy 1 TACCATGAGGACAAATATCTTTTGGAGGACAAACAGTCTACCACTCTCTTTTCAGCAA 60

Db 15144 TCCCGTGAGGCCAAATATCTTCTGAGGGGCCAGATTAATACAACTTACTATCCGCCA 15203

Qy 61 TCCCATACATCGGTACAAACCTAGTGTAGATGAATCTGTAGAGGGTCTCTAGTAGATAAG 120

Db 15204 TCCCATACATTTGGGACAGACCTAGTTCATGAATCTGTAGAGGGTCTCTAGTAGAGTC 15263

Qy 121 CAACCTTACCGGATTTTTCGGCTTCCACTTTATCTCTCCCACTTATCTATCTGAGCCCTTA 180

Db 15264 CCACCTTACAGGATTTCTTACCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 15323

Qy 181 CCATAGTACACTACTGTCTTCTCCACGAAACAGGATCCAAACCCACAGCAATCTCTAT 240

Db 15324 CAACACTCCACTCTCTATTTCTGACGAAACGGATCAAAACACCCCTAGGATCACT 15383

Qy 241 CAGACGAGACAAATTCCTATTCACCCCTACTACACTATCAAGATATCTTAGAGCTC 300

Db 15384 CCCATTCGATAAAATCACCTTCCACCTTACTACAAATCAAAAGACGCCCTCGGCTTAC 15443

Qy 301 TACTATTAATTTAAACCTCATGCTTCTAGTCTCTTCTCTACCGGACCTGTTGGAGACC 360

Db 15444 TTCT 15503

Qy 361 CAGACAACTATACACGACCAACCCCTTATATACACCCCACTATCAAGCCCAATGAT 420

Db 15504 CAGACAAATATACCTAGCCAAACCCCTTAAACACCCCTCCCACTCAAGCCCAATGAT 15563

Qy 421 ACTTCCTATTGGATAGCAATCTCTCGATCAATCTCTCAAACTAGGAGG 472

Db 15564 ATTTCCTATTGCGCTACACAAATTCCTCGATCGCTCCCTTAACAAACTAGGAGG 15615

RESULT 7

US-09-377-497-7

; Sequence 7, Application US/09377497

; Patent No. 6670119

; GENERAL INFORMATION:

; APPLICANT: YOSHIKAWA, YOSHIE

; APPLICANT: MUKAI, HIROYUKI

; APPLICANT: ASADA, KIYOZO

; APPLICANT: HINO, FUMITSUGU

; APPLICANT: KATO, IKUNOSHIN

; TITLE OF INVENTION: CANCER-ASSOCIATED GENES

; FILE REFERENCE: 1422-388P

; CURRENT APPLICATION NUMBER: US/09/377,497

; CURRENT FILING DATE: 1999-08-20

; NUMBER OF SEQ ID NOS: 70

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 7

; LENGTH: 1140

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: any n or Xaa = unknown

US-09-377-497-7

Query Match 60.3%; Score 284.8; DB 4; Length 1140;

Best Local Similarity 75.2%; Pred. No. 4.5e-86;

Matches 355; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

Qy 1 TACCATGAGGACAAATATCTTTTGGAGGACAAACAGTCTACCAATCTCTTTTCAGCAA 60

Db 398 TCCCGTGAGGCCAAATATCTTCTGAGGGGCCAGATTAATACAACTTACTATCCGCCA 457

Qy 61 TCCCATACATCGGTACAAACCTAGTGTAGATGAATCTGTAGAGGGTCTCTAGTAGATAAG 120

Db 458 TCCCATACATTTGGGACAGACCTAGTTCATGAATCTGTAGAGGGTCTCTAGTAGAGTC 517

Qy 121 CAACCTTACCGGATTTTTCGGCTTCCACTTTATCTCTCCCACTTATCTATCTGAGCCCTTA 180

Db 518 CCACCTTACAGGATTTCTTACCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 577

Qy 181 CCATAGTACACTACTGTCTTCTCCACGAAACAGATCCAAACCCACAGCAATCTCTAT 240

Db 578 CAGCACTCCACTCTCTATTTCTGACGAAACGGATCAAAACCCCTAGGATCACT 637

Qy 241 CAGACGAGACAAATTCCTATTCACCCCTACTACACTATCAAAAGATATCTTAGAGCTC 300

Db 638 CCCATTCGATAAAATCACCTTCCACCTTACTACAAATCAAAAGACACCTCTCGCTTAC 697

Qy 301 TACTATTAATTTAAACCTCATGCTTCTAGTCTCTTCTCTACCGGACCTGTTGGAGACC 360

Db 698 TTCT 757

Qy 361 CAGACAACTATACACGACCAACCCCTTATATACACCCCACTATCAAGCCCAATGAT 420

Db 758 CAGCAATATATACCTAGCCAAACCCCTTAAACACCCCTCCCACTCAAGCCCAATGAT 817

Qy 421 ACTTCCTATTGCTAGGCAATCTCTCGATCAATCTCTTAACAAACTAGGAGG 472

Db 818 ATTTCCTATTGCGCTACACAAATTCCTCGATCGCTCCCTTAACAAACTAGGAGG 869

RESULT 8

US-09-385-982-185

; Sequence 185, Application US/09385982

; Patent No. 6262334

; GENERAL INFORMATION:

; APPLICANT: ENERGE, WILSON O., ET AL.

; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION

; FILE REFERENCE: CCNDA-260XX

; CURRENT APPLICATION NUMBER: US/09/385,982

; CURRENT FILING DATE: 1999-08-30

; EARLIER APPLICATION NUMBER: 09/328,111

; EARLIER FILING DATE: 1999-06-08

; EARLIER APPLICATION NUMBER: 60/117,393

; EARLIER FILING DATE: 1999-01-27

; EARLIER APPLICATION NUMBER: 60/098,639

; EARLIER FILING DATE: 1998-08-31

; NUMBER OF SEQ ID NOS: 544

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 185

```

; LENGTH: 614
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)-(614)
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-185

Query Match      41.3%; Score 195; DB 3; Length 614;
Best Local Similarity 73.3%; Pred. No. 6.9e-56;
Matches 263; Conservative 0; Mismatches 95; Indels 1; Gaps 1;

QY 114 GATAAGCAACCTTACCGATTTTCGGCTTCCACTTATCTCCCATTTATCGCA 173
Db      8 GACAGTCCACCTCCACAGATTTTACCTTTTCACTTTTCACTTGGCCCTTCATTATGCA 67

QY 174 GCCCTTACCATAGTACACCTAGTCTGTTTCTCCACGAAACAGGATCCAAACCCCAAGGA 233
Db      68 GCCCTAGAGCACTCACCTCTATTTCTTGACGAAACGGGATCAACACCCCTTAGGA 127

QY 234 ATCTCATCAGACGACAGCAAAATTCATTCACCCCTACTACACTATCAAGATATCTTA 293
Db      128 ATCACTCCATTCGGATAAATCACCTTCCACCTTACTACAAATCAAGAGCGCCTC 187

QY 294 GGAGCTCTACTATTAATTTTAAACCTCAGCTTCTAGTCTTATCTCACCGGACCTGCTT 353
Db      188 GGCTTACTTCTCTCTCTCTCTCTTAATGACATTAACACTATTTCTCACGAGACCTCTTA 247

QY 354 GGAGACCCAGACACTATACACGACAAACCCCACTTAAATACACCCCAATATCAAGCCC 413
Db      248 GCGACCCAGACAATTAATACCTAGGCAACCCCTTAAACACCCCTCCACATCAAGCCC 307

QY 414 GAATGATATCTCTATTTGCATACGCAATCTCCGATCAATTTCTTAACAACTAGGAGG 472
Db      308 GAATGATATTTCTATTCGCTACACAATTTCTTGATC-CGTCTTAAACAACTAGAGG 365

RESULT 9
US-09-385-982-493/c
; Sequence 493, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCDNA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; EARLIER FILING DATE: 1999-08-30
; EARLIER FILING DATE: 1999-06-08
; EARLIER FILING DATE: 1999-01-27
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 493
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(591)
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-493

Query Match      38.6%; Score 182; DB 3; Length 591;
Best Local Similarity 71.4%; Pred. No. 1.7e-51;
Matches 250; Conservative 0; Mismatches 99; Indels 1; Gaps 1;

QY 124 CCCTTACCGATTTTCGGCTTCCACTTATCTCCCATTTATCATTTATCATTCGAGCCCTTACCA 183

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Db      548 CCNTCACNMGATNTTTTACCTTTTCACTTTTGGCCTTCATTATGACAGCCCTTAGCAG 489
QY 184 TAGTACACCTACTGTTTCTC-CAGAAACAGATCCAAACACCCACAGGATCTCATCA 242
Db      488 CATTCCACTTCTTATTTCTTGAGAGAAACGGGATCAACACCCCTTAGGAATCACTCC 429
QY 243 GACGACAGCAAAATTTCCATTTCCACCCCTACTACACTATCAAGATATCTTAGAGCTCTA 302
Db      428 CATTCCGATAAATCACTCTTCCACCCCTTACTACACAATCAAGAGCGCCTCGGCTTACTT 369
QY 303 CTATTAATTTAAACCTCATGCTTCTAGTCTTCTTCTCACCGGACCTGCTTGGAGACCA 362
Db      368 CTCCTCTCTCTCTCTCTTAAATGACATTAACACTATTTCTCACGAGACCTCTTAGGCGACCA 309
QY 363 GACAACTATACACGACAAACCCACTTAAATACACCCCACTATCAAGCCCAATGATAC 422
Db      308 GACAATTAATACCTAGCAACCCCTTAAACACCCCTCCCATCAACAACTAGGAGG 249
QY 423 TTCTTATTTGCATCGCAATCTCCGATCAATTTCTTAACAACTAGGAGG 472
Db      248 TTCTTATTTGCCTACACAATTTCTCGATCCGTCCTTAAACAACTAGGAGG 199

RESULT 10
US-09-385-982-375/c
; Sequence 375, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCDNA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; EARLIER FILING DATE: 1999-08-30
; EARLIER FILING DATE: 1999-06-08
; EARLIER FILING DATE: 1999-01-27
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 375
; LENGTH: 602
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(602)
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-375

Query Match      38.1%; Score 179.6; DB 3; Length 602;
Best Local Similarity 65.8%; Pred. No. 1.1e-50;
Matches 265; Conservative 0; Mismatches 137; Indels 1; Gaps 1;

QY 71 CGGTACAAACCTAGTAGAATGAATCTCGAGAGGGTCTCAGTAGATAAAGCAACCCCTTAC 130
Db      601 CCGGCAAGTTNCGGGCAATGATTTTAGGANGTTATCAGTAAACAGTCCACCCCTTAN 542
QY 131 CGGATTTTTCGCTTCCACTTTATCTCCCATTTATCTTCGATTTATCGAGCCCTTACCATAGTACA 190
Db      541 GGTNTTNTTACCTTTCAAATTCATTNTGCCNTTCATTTTGAAGCCNTAAGAAGCATTC 482
QY 191 CCTACTGTTTCTC-CAGAAACAGGATCCAAACCCCAAGGAATCTCATCAGAGCGAG 249
Db      481 ACTTCNTATTTCTGGCACAAACGGGGNTCAACANCCCTTAGNAATCACTTCCCATTCOG 422
QY 250 ACAAATTCATTCACCCCTTACTACACTATCAAGATATCTTAGGAGCTCTTACTATTAA 309
Db      421 ATAAATTCACCTTCCACCCCTTACTACACAATCAAGAGCGCCCTCGGCTTACTTCTTTCA 362
QY 310 TTTTAAACCTCATGCTTCTAGTCTTCTTCTCACCAGACCTGCTTTGGAGACCCAGCAACT 369

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Db 361 TTCTCTCTTAATGACATTAAACATATTCTCACCAGAGCTCTAGCGACCCAGACAATT 302
Qy 370 ATACACGAGCAACCCCTTAATACACCCACATATCAAGCCGGAATGATCTTCTTAT 429
Db 301 ATACCTAGCCAAACCCCTTAACACCCCTCCCAATCAAGCCGGAATGATTTCTTAT 242
Qy 430 TTGCATAGCAATCTCCGATCAATTCCTTAACAACTAGGAGG 472
Db 241 TCGCTACACAATCTCCGATCCGTCCTTAACAAGCTAGGAGG 199

RESULT 11

US-09-385-982-510/c
; Sequence 510, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CDNA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; EARLIER FILING DATE: 1999-08-30
; EARLIER FILING DATE: 1999-06-08
; EARLIER FILING DATE: 1999-01-27
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 510
; LENGTH: 619
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(619)
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-510

Query Match 31.7%; Score 149.4; DB 3; Length 619;
Best Local Similarity 68.0%; Pred. No. 1.7e-40;
Matches 230; Conservative 0; Mismatches 105; Indels 3; Gaps 2;

Qy 136 TTTTCGGCTTCCACTTTATCTCCCATTTATCAATTGAGCCCTTACCATAGTACACCTAC 195
Db 534 TTTTTCCTTTCAATTATTTATGTC--TTCAATTATGAGCCCTAGCAGCATTCCTTCT 477
Qy 196 TGTTTCCAGAAACAGGATCCAAACACCCACAGGAATCTCATCAGACGACACAAA 255
Db 476 TATTTTGGCACGAAAGGATCAAAACCAACCCCTTAGNAATCACTTCCATTTCNGATAAA 417
Qy 256 TTCCATTCCACCCCTACTACACTATCAAGATATCTTAGGAGCTCTACTAATTTT-TA 314
Db 416 TCAGTTTCCACCTTANTACAAATCAAGACGCCCTCGGGCTTATTTTTTCTTCTC 357
Qy 315 ACCCTCATGCTTCTAGTCCTTATCTCAGCCGACCTGCTTGAGACCCAGACAACTACA 374
Db 356 TCNTTAATGACATTAAACATATTCTCAGACACTCTTAGGGAGCCAGACAATTAACC 297
Qy 375 CAGCAAAACCCCTTAATACACCCCAATATCAAGCCCGAATGATCTTCTTATTTGCA 434
Db 296 CTAGCCAAACCCNTTAAACACCCCTCCCAATCAAGCCCGAATGATTTCTTATGGCC 237
Qy 435 TAGCAATCTCCGATCAATTCCTTAACAACTAGGAGG 472
Db 236 TACAAATTCGATCCGTCCTTAAACAACTAGGAGG 199

RESULT 12

US-09-328-111-763/c
; Sequence 763, Application US/09328111

; Patent No. 6262333
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O.
; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Derti, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS
; FILE REFERENCE: CCD-257 (US)
; CURRENT APPLICATION NUMBER: US/09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: US 60/088,801
; EARLIER FILING DATE: 1998-06-10
; NUMBER OF SEQ ID NOS: 850
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 763
; LENGTH: 578
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(578)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-111-763

Query Match 30.9%; Score 146; DB 3; Length 578;
Best Local Similarity 74.0%; Pred. No. 2.4e-39;
Matches 196; Conservative 0; Mismatches 68; Indels 1; Gaps 1;

Qy 209 AACAGGATCCAAACACCCACAGGAATCTCATCAGACGACAAATTCATTCACCC 268
Db 569 AACGGATCAACCAACCCCTTAGGAATCACTCCCATCCGATAAATCACTTCCACCC 510
Qy 269 CTACTACACTATCAAGATATCTTAGGAGCTCTAC-TATTAAATTTTAAACCTCATGCTTC 327
Db 509 TTANTACAAATCAAGACGCCCTTAGGCTTACTTCTTCTCTCTCTCTTAAATGACAT 450
Qy 328 TAGTCTTATCTCAGCGAGCTGCTTGAGACCCAGACACTATACACGACAAACCCAC 387
Db 449 TAACTACTATTCTCACCAGACCTTNTAGGCGACCCAGACAATTATACCTTAGCCACCCCT 390
Qy 388 TTAATACACCCCAACATATCAAGCCCAATGATATCTTCTTATTTGATAGCAATCTCTCC 447
Db 389 TAAACACCCCTCCCAACATCAAGCCCAATGATATTTCTTATTCGCTTACAAATTTCTCC 330
Qy 448 GATCAATTCCTTAACAACTAGGAGG 472
Db 329 GATCCGTCCTTAAACAACTAGGAGG 305

RESULT 13

US-09-328-111-562/c
; Sequence 562, Application US/09328111
; Patent No. 6262333
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O.
; APPLICANT: Steinmann, Kathleen E.
; APPLICANT: Astle, Jon H.
; APPLICANT: Burgess, Christopher C.
; APPLICANT: Bushnell, Steven E.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Catino, Theodore J.
; APPLICANT: Derti, Adnan
; APPLICANT: Ford, Donna M.
; APPLICANT: Lewis, Marcia E.

APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 562
LENGTH: 597
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(597)
OTHER INFORMATION: n = A,T,C or G
US-09-328-111-562

Query Match 27.6%; Score 130.4; DB 3; Length 597;
Best Local Similarity 62.8%; Pred. No. 4.5e-34;
Matches 246; Conservative 0; Mismatches 134; Indels 12; Gaps 4;
QY 93 ATCTGAGGAGGTTCTCAGTAGAAGCAACCTTACCGGATTTTTCGCC-----TT 145
DB 596 ATTTTAGGGGGTTCTCANNANACGTCCCGCCCNNTNNAAGNTTTTTTNNCNWTTCAATT 537
QY 146 CCACCTTTATCTCCCATTTATCATTCAGCCCTTACCATAGTACACTACTGTTTCTCCA 205
DB 536 TAAATTTGGCCNTAATATATGNGCCNANNNGAAATTCACNTCCANTTTANGGCAN 477
QY 206 CGAAACAGGATCAACCAACCCAC--AGGAATCTCATAGACGACGACAAATTCATTC 263
DB 476 GAAAGGGNNTCAACCAACCCCTTCTAGNATCACTTCCCATTCGCGATAAAATCACTTTC 417
QY 264 CACCCC-TACTACTATCAAGATATCTTAGAGCT--CTACTATTAATTTTAAACCTTC 320
DB 416 CACCCCTTACTACAAATCAAGACGCGCCCTCGGGCTTACTTCTCTCTCTCTCTCTTA 357
QY 321 ATGCTTCTAGTCTTCTTCTCAGCGACCTGCTTGGAGACCCAGACAACTATACACAGCA 380
DB 356 ATGACATTAACACTATTTCTACAGACCTCTTAGGCGCCAGACAAATATACCTTAGCC 297
QY 381 AACCCACTTAATACACCCCAATATCAAGCCCGAATGATCTTCTTATTTGATACGCA 440
DB 296 AACCCCTTAAACACCCCTTCCCAATCAAGCCCGAATGATATTTCTTATTCGCTACACA 237
QY 441 ATCTCTCGATCAATTTCTTAACTAGGAGG 472
DB 236 ATTCTCGATCGCTCCCTTAACTAGGAGG 205

RESULT 14
US-08-998-416-190/c
Sequence 190, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jürgen
APPLICANT: Knechtle, Philipp
APPLICANT: Reibschung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
NUMBER OF INVENTION: AND USES THEREOF
CORRESPONDENCE ADDRESS:
ADDRESS: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park

STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 190:
SEQUENCE CHARACTERISTICS:
LENGTH: 650 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1076RP
US-08-998-416-190

Query Match 27.1%; Score 127.8; DB 3; Length 650;
Best Local Similarity 55.2%; Pred. No. 3.5e-33;
Matches 249; Conservative 0; Mismatches 202; Indels 0; Gaps 0;
QY 1 TACCATGAGGACAAATATCTTTTGGAGGACCAAGTCATCACCATCTCTCTTTCAGCAA 60
DB 451 TAGTATATGACAAATGTCACATTTAGGTTGCTACTGTTTATTACTAATTTATTAGTGCTA 392
QY 61 TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGAGGGTTTCTCAGTAGATAAAG 120
DB 391 TTCCATTTTATGGAAATGATTTGTACTATGATTATGAGGATCATTTAGTTAGTAATC 332
QY 121 CACCCCTTACCGATTTTTCGGCTTCCACTTTTATCTCCGATTTATCATTGCGAGCCCTTA 180
DB 331 CTACTATTATAAGATTTCTTTCTATTTCATTTATTAGTACCATTTATTATTGCGCAATAG 272
QY 181 CCATAGTACACCTTACTGTTTCTCCAGAAACAGGATCCCAACCCACAGGAATCTCAT 240
DB 271 TAAATTAAGATTTAATGCTATTACATGATGTTTCAATCAATCCATTAGGTATTACAG 212
QY 241 CAGACGACAGACAAATTTCCATTCACCCCTTACACTATCAAGATATCCTTAGGAGCTC 300
DB 211 GTAAATTTAGATAGATTACCAATGCTGTTTATTTTAAAGATTTAGTAACAGTAT 152
QY 301 TACTATTAAATTTAAACCTCATGCTTCTAGTCTCTATCTCACCAGGACCTGCTTTGGAGACC 360
DB 151 TTGTAATTTAAATTTCTTTTTCATTTTGTATTTCTTTTTCACCTAATCTTTTAGGACATC 92
QY 361 CAGACAACTATACACAGCAAAACCCACTTAATACACCCCAATATCAAGCCCGAATGAT 420
DB 91 CTGATAATTTATATTCAGGTAATCTTTTAGTACACAGCATCTATTGTACCTGAATGAT 32
QY 421 ACTTCCTATTGTCATACGCAATCTCCGATC 451
DB 31 ATTATTACCATTTCTATCTATTTTTAAGATC 1

RESULT 15
US-08-998-416-1032/c
Sequence 1032, Application US/08998416

Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgan
APPLICANT: Knechtle, Philipp
APPLICANT: Reibschung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPHII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 1032:
SEQUENCE CHARACTERISTICS:
LENGTH: 716 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
ORGANISM: PAG1631UP
US-08-998-416-1032

Query Match 27.1%; Score 127.8; DB 3; Length 716;
Best Local Similarity 55.2%; Pred. No. 3.7e-33;
Matches 249; Conservative 0; Mismatches 202; Indels 0; Gaps 0;
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Db 451 TAGTATATGGCAAAATGTCATTTGAGTGCTACTGTATTACTAAATTTATTAGTGCTA 392
QY 61 TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTCTCTCAGTAGATAAG 120
Db 391 TTCCATTTATGGAAATGATATTTGCTACTATGATTTATGAGGATCAATTTAGTGTAGTAATC 332
QY 121 CAACCCCTTACCCGATTTTTCGCTTCCACTTTATCTCCCATTTTATCATTTGACGCCCTTA 180
Db 331 CTACTATTATAAGATTTCTTCTTCAATTTATTAGTACCAATTTATTATTGCGCAATAG 272
QY 181 CCATAGTACACCTACTGTCTTCCAGCAACAGGATCCACCAACCCACAGGATCTCAT 240
Db 271 TAAATATGCATTTAATGCTATTATACATGATGTTTATCAATCCATCCATTAGGTATTACAG 212
QY 241 CAGACGCGACAAATTCATTTCCACCCCTACTACACTATCAAAAGATATCCTAGGAGCTC 300
Db 211 GTAATTTAGATAGATTACCAATGCATGGTATTATTTTAAAGATTTAGTAACAGTAT 152

QY 301 TACTATTAAATTTTAACCCCTCATGCTTCTAGTCCTATTCTCACCGGACCTGCTTGGAGACC 360
Db 151 TTGTAATTTATAAATTTCTTTTCAATTTATTGTTATCTTTTACCTTAATCTACTTTAGGACATC 92
QY 361 CAGACAACCTATACACCCAGCAAAACCCACCTTAATATACACCCCAATATCAAGCCCGAATGAT 420
Db 91 CTGATAATTAATATCCAGGTAATCCTTTAGTAACACACGAGCATCTATTGCTACCTGAATGAT 32
QY 421 ACTTCCTATTGTCATACGCAATCTCCGATC 451
Db 31 ATTTATTACCAATCTATCTTATTTTTAAGATC 1

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Job time : 169.862 secs

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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 23:47:45 ; Search time 703.939 Seconds
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3621.431 Million cell updates/sec

Title: US-09-821-782E-48

Perfect score: 472

Sequence: 1 taccatggaggcaaatatct.....attcctaacaactaggagg 472

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3625171 seqs, 2700493622 residues

Total number of hits satisfying chosen parameters: 7250342

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	318.4	67.5	16300	16	US-10-191-803-11
2	315.2	66.8	1912	16	US-10-191-803-2
3	311	65.9	416	9	US-09-960-352-12545
4	308.2	65.3	411	9	US-09-960-352-3407
5	308	65.3	412	9	US-09-960-352-9822
6	301.6	63.9	448	9	US-09-960-352-8757
7	288	61.0	16569	16	US-10-308-264-370
8	288	61.0	16569	16	US-10-308-264-479
9	288	61.0	16570	16	US-10-308-264-213
10	288	61.0	16572	16	US-10-308-264-287
11	286.4	60.7	16559	16	US-10-308-264-150
12	286.4	60.7	16559	16	US-10-308-264-214

13	286.4	60.7	16559	16	US-10-308-264-221
14	286.4	60.7	16560	16	US-10-308-264-373
15	286.4	60.7	16561	16	US-10-308-264-206
16	286.4	60.7	16561	16	US-10-308-264-264
17	286.4	60.7	16562	16	US-10-308-264-180
18	286.4	60.7	16562	16	US-10-308-264-420
19	286.4	60.7	16563	16	US-10-308-264-448
20	286.4	60.7	16563	16	US-10-308-264-448
21	286.4	60.7	16564	16	US-10-308-264-199
22	286.4	60.7	16564	16	US-10-308-264-204
23	286.4	60.7	16564	16	US-10-308-264-326
24	286.4	60.7	16564	16	US-10-308-264-376
25	286.4	60.7	16565	16	US-10-601-692-1
26	286.4	60.7	16568	16	US-10-308-264-367
27	286.4	60.7	16568	16	US-10-308-264-480
28	286.4	60.7	16568	16	US-10-308-264-548
29	286.4	60.7	16568	16	US-10-308-264-561
30	286.4	60.7	16569	9	US-09-098-079-2
31	286.4	60.7	16569	13	US-10-053-611-1
32	286.4	60.7	16569	16	US-10-308-264-1
33	286.4	60.7	16569	16	US-10-308-264-11
34	286.4	60.7	16569	16	US-10-308-264-477
35	286.4	60.7	16569	16	US-10-308-264-495
36	286.4	60.7	16569	16	US-10-308-264-499
37	286.4	60.7	16569	16	US-10-308-264-502
38	286.4	60.7	16569	16	US-10-308-264-510
39	286.4	60.7	16569	16	US-10-308-264-516
40	286.4	60.7	16569	16	US-10-308-264-526
41	286.4	60.7	16569	16	US-10-308-264-527
42	286.4	60.7	16569	16	US-10-308-264-531
43	286.4	60.7	16569	17	US-10-361-002-10
44	286.4	60.7	16569	17	US-10-361-004-10
45	286.4	60.7	16569	17	US-10-361-004-10

ALIGNMENTS

RESULT 1

US-10-191-803-11
; Sequence 11, Application US/10191803
; Publication No. US20040014040A1
; GENERAL INFORMATION:
; APPLICANT: MENDRICK, Donna
; APPLICANT: PORTER, Mark
; APPLICANT: JOHNSON, Kory
; APPLICANT: HIGGS, Brandon
; APPLICANT: CASTLE, Arthur
; APPLICANT: ELASHOFF, Michael
; TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5090US
; CURRENT APPLICATION NUMBER: US/10/191,803
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/303,819
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/305,623
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/369,351
; PRIOR FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: US 60/377,611
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 1140
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 11
; LENGTH: 16300
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20040014040A1 X14848
US-10-191-803-11

Query Match 67.5%; Score 318.4; DB 16; Length 16300;
Best Local Similarity 79.7%; Pred. No. 1.2e-88;

Matches 376; Conservative 0; Mismatches 96; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCTTTTGGAGGACAAAGTTCATCACCAATCTCTTTTACGCAA 60
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14521 TCCCATGAGGACAAATATCTTTGAGGAGCTACAGTAATTAACAACCTATTATCAGCTA 14580
QY |||||
61 TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTTCTCAGTAGATAAAG 120
Db |||||
14581 TCCCTTACATTTGGGACTACCTTAGTCGAATGAATCTGAGGAGGGTTCTCAGTAGACAAG 14640
QY |||||
121 CAACCTTACCGGATTTTTCGCTTCCACTTATATCTCCCTATATCATTTGAGGCCCTTA 180
Db |||||
14641 CAACCTTAAACGGTCTTCTGCAATTTCCACTTCATCTCCCTCATTTATATCGCGGCCCTTG 14700
QY |||||
181 CCATAGTACACTACTGTTTCTCCACGAAACAGGATCCAAACCCACAGCAATCTCAT 240
Db |||||
14701 CAATGTACATCTTCTTCTCCACGAAACAGGATCAATAACCCACAGGATTAACACT 14760
QY |||||
241 CAGACGCAGACAAATTCATTCACCCCTACTACACTATCAAAAGATATCTTAGGAGCTC 300
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14761 CCGACGCAGACAAATCCATTCATCCATCATATTATACAAATTAAGACCTCTTAGTGTAT 14820
QY |||||
301 TACTATTAATTTAAACCTCATGCTTCTAGTCTTATCTTCAACCGGACCTGTTGGAGACC 360
Db |||||
14821 TTATATTACTATTATCTCTTAATAACCTTAGTACTATTCTTCCAGACCTACTAGGAGACC 14880
QY |||||
361 CAGACAACTATACACCGCAACCCACTTAATACACCCCAACATATCAAGCCCAATGAT 420
Db |||||
14881 CAGCAATTAACACCGCTCAACCCCTCAACACCCCAACATCAACCAAGATGAT 14940
QY |||||
421 ACTTCTTATTTGATAGCAATCTCCGATCAATTCCTTAACAAACTAGGAGG 472
Db |||||
14941 ACTTCTTCTTGGCTAGCTATTCTAGCTCCATTCACCAAACTAGGAGG 14992

RESULT 2

US-10-191-803-2
; Sequence 2, Application US/10191803
; Publication No. US20040014040A1
; GENERAL INFORMATION:
; APPLICANT: MENDRICK, Donna
; APPLICANT: PORTER, Mark
; APPLICANT: JOHNSON, Kory
; APPLICANT: HIGGS, Brandon
; APPLICANT: CASTLE, Arthur
; APPLICANT: ELASHOFF, Michael
; TITLE OF INVENTION: Cardiotocin Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5090US
; CURRENT APPLICATION NUMBER: US/10/191,803
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/303,819
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/305,623
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/369,351
; PRIOR FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: US 60/377,611
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 1140
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1912
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20040014040A1 J01436
US-10-191-803-2

Query Match 66.8%; Score 315.2; DB 16; Length 1912;
Best Local Similarity 79.2%; Pred. No. 4.5e-88;
Matches 374; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCTTTTGGAGGACAAAGTTCATCAACCAATCTCTCTTTCAGCAA 60

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QY |||||
61 TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTTCTCAGTAGATAAAG 120
Db |||||
769 CCCCTTACATTTGGGACTACCTTAGTCGAATGAATCTGAGGAGGGTTCTCAGTAGACAAG 828
QY |||||
121 CAACCCCTTACCGGATTTTTCGCTTCCACTTATATCTCCCTATATCATTTGAGGCCCTTA 180
Db |||||
829 CAACCCCTTAAACGGTCTTCTTCCATTTCCACTTCATCTCTCCCTCATTTATATCGCGGCCCTTG 888
QY |||||
181 CCATAGTACACTACTGTTTCTCCACGAAACAGGATCCAAACCCACAGCAATCTCAT 240
Db |||||
889 CAATGTACATCTTCTTCTCCACGAAACAGGATCAATAACCCACAGGATTAACACT 948
QY |||||
241 CAGACGCAGACAAATTCATTCACCCCTACTACACTATCAAAAGATATCTTAGGAGCTC 300
Db |||||
949 CCGACGCAGACAAATCCATTCATCCATCATATTATACAAATTAAGAAGCTCTAGTGTAT 1008
QY |||||
301 TACTATTAATTTAAACCTCATGCTTCTAGTCTTATCTTCAACCGGACCTGTTGGAGACC 360
Db |||||
1009 TTATATTACTATTATCTCTTAATAACCTTAGTACTATTCTTCCAGACCTACTAGGAGACC 1068
QY |||||
361 CAGACAACTATACACCGCAACCCACTTAATACACCCCAACATATCAAGCCCAATGAT 420
Db |||||
1069 CAGCAATTAACACCGCTCAACCCCTCAACACCCCAACATCAACCAAGATGAT 1128
QY |||||
421 ACTTCTTATTTGATAGCAATCTCCGATCAATTCCTTAACAAACTAGGAGG 472
Db |||||
1129 ATTTTCTCTTGGCTAGCTATTCTAGCTCCATTCACCAAACTAGGAGG 1180

RESULT 3
US-09-360-352-12545
; Sequence 12545, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 12545
; LENGTH: 416
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (409)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 54-BOVMS1-020-Q1-E1-F10
US-09-360-352-12545

Query Match 65.9%; Score 311; DB 9; Length 416;
Best Local Similarity 84.1%; Pred. No. 4.7e-87;
Matches 350; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

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1 CAGCAATCCCATACATCGGCACAAATTTAGTCAATGAATCTGAGGCGGATTTCTCAGTAG 60
QY |||||
115 ATAAAGCAACCCCTTACCCGATTTTTCGCTTTCCTTCCACTTATCTCTCCCACTTATCATTCAG 174
Db |||||
61 ACAAGCAACCCCTTACCCGATTTCTCGCTTTCCTTCCATTTATCTTCCATTCATCATAG 120
QY |||||
175 CCCTTACCATAGTACACTACTGTTTCTCCACGAAACAGGATCCAAACCCCAACAGGAA 234
Db |||||
121 CAATTGCCATAGTCCACTACTATTCTCTCCACGAAACAGGCTCCCAACCAACCAACAGGAA 180

QY 235 TCTCATCAGCCGACGAAATTCATTCACCCCTACTACACTATCAAGATATCCTAG 294
DB 181 TTTCCTCAGAGTAGCAAAATCCCATTCACCCCTACTATACCAATTAAGACATCTTAG 240
QY 295 GAGCTCTACTATTAATTTAAACCTCATGCTTCTAGTCTTCTATTCACCGGACCTGCTTG 354
DB 241 GGGCCCTCTTACTAATCTAGCTCTAATCTACTAGTACTATTTCGACCCCGACCTCCTCG 300
QY 355 GAGACCCGACAACTATACACAGCAAAACCCCACTTAATATACACCCCAACATATCAAGCCCG 414
DB 301 GAGACCCGACAACTATACACAGCAAAACCCCACTTAATATACACCCCAACATATCAAGCCCG 360
QY 415 AATGATACTCTTATTCATACGCAATCTCGATCAATTCCTAATCAAACTAGGA 470
DB 361 AGTGATACTCTTATTTGATACGCAATCTTAGATCAATGCAACCAACTAGGA 416

RESULT 4
US-09-960-352-3407
; Sequence 3407, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 3407
; LENGTH: 411
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (289)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 15-LIB34-003-Q1-E1-D11
US-09-960-352-3407

Query Match 65.3%; Score 308.2; DB 9; Length 411;
Best Local Similarity 84.4%; Pred. No. 3.6e-86;
Matches 346; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 6 TGAGGACAAATATCTTTTGGAGGACAAACAGTCAACCAATCTCCTTTTCAGCAATCCCA 65
DB 1 TGAGGACAAATATCAITCTGAGGAGCAACAGTCAACCAATCTCCTTTTCAGCAATCCCA 60
QY 66 TACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGTTCTCAGTAGAATAAGCAAC 125
DB 61 TACATCGGCACAAATTTAGTGGAAATGAATCTGAGGCGGATTTCTCAGTAGAATAAGCAAC 120
QY 126 CTTACCGGATTTTGGCTTCGATTTATCTCCGATTTATCTCAGTTCAGGCGCTTACATA 185
DB 121 CTTACCGGATTTTGGCTTCGATTTATCTCCGATTTATCTCAGTTCAGGCGCTTACATA 180
QY 186 GTACACTACTGTTTCTCCAGGAAACAGGATCAACAAACCCCAAGAAATCTCATCAGAC 245
DB 181 GTCCACCTACTATTTCTCCAGGAAACAGGATCAACAAACCCCAAGAAATTTCTCAGAC 240
QY 246 GCAGACAAATTCATTCACCCCTACTACACTATCAAGATATCTCAGGAGCTCTACTA 305
DB 241 GTAGACAAATTCATTCACCCCTACTATACCAATTAAGGACATCTTANGGCGCTCTTA 300
QY 306 TTAATTTAAACCTCATGCTTCTAGTCTTATCTCAGGAGACCTGCTTGGAGACCCGAC 365
DB 301 CTAATTTAGTCTTAATCTACTAGTACTATTGCGACCCGACCTCTCTCGGAGACCCGAC 360
QY 366 AACTATACACGCAAAACCCACTTAATACACCCCAACATATCAAGCCCGA 415

DB 361 AACTATACACCCGCAATCCACTCAACACACCCCTCTCATCAAAACCGGA 410

RESULT 5
US-09-960-352-9822
; Sequence 9822, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 9822
; LENGTH: 412
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 42-LIB34-012-Q1-E1-C10
US-09-960-352-9822

Query Match 65.3%; Score 308; DB 9; Length 412;
Best Local Similarity 84.2%; Pred. No. 4.1e-86;
Matches 347; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 36 GTCATCACCACATCTCTTTTCAGCAATCCCATACATCGGTACAAACCTAGTAGAATGAATC 95
DB 1 GTCATCACCACATCTCTTTTCAGCAATCCCATACATCGGTACAAACCTAGTAGAATGAATC 60
QY 96 TGAGGAGGTTCTCAGTAGATAAGCAACCTTACCCGATTTTTCGCTTCCACTTTATC 155
DB 61 TGAGGCGGATTTCTCAGTAGATAAGCAACCTTACCCGATTTTTCGCTTCCACTTTATC 120
QY 156 CTCCCATTTATCATTCGAGCCCTTACCATAGTACACTACTGTTCTCCACGAAACAGGA 215
DB 121 CTTCCATTTATCATCATAGCAATTTGCCATAGTCCACTACTATTTCTCCAGAAACAGGC 180
QY 216 TCCACAAACCCCAACAGGAATCTCATCAGACGAGCAAAATTCATTCACCCCTACTAC 275
DB 181 TCCACAAACCCCAACAGGAATTTCTTCAGAGCTAGACAAATTCATTCACCCCTACTAT 240
QY 276 ACTATCAAGATATCTCAGGAGTCTACTATTAATTTTAACTCTCATGCTTCTAGTCTTA 335
DB 241 ACCATTAAAGGACATCTTAGGGCCCTCTTACTAATTTCTAGTCTTAATCTACTAGTACTA 300
QY 336 TTTCTACCCGAGCTGCTTCGAGACCCAGACAACTATACACCCAGCAAAACCCACTTAATACA 395
DB 301 TTGCGACCCGAGCTCTCTCGAGACCCAGATTAATACACCCAGCAATTCCTCAACACA 360
QY 396 CCCCCACATATCAAGCCCGAATGATATCTTCTATTTGATACGCAATCTCTCC 447
DB 361 CCCCCACATCAAAACCCGAGTACTTCTTATTGATACGCAATCTTAC 412

RESULT 6
US-09-960-352-8757
; Sequence 8757, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24

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; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 8757
; LENGTH: 448
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 38-BOVMS1-021-Q1-E1-B6
US-09-960-352-8757

Query Match      63.9%; Score 301.6; DB 9; Length 448;
Best Local Similarity 84.2%; Pred. No. 4.4e-84;
Matches 340; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 69 ATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTCTCAGTAGATAAAGCAACCCCTT 128
Db 1 ATCGGCACAAATTTAGTCGAATGAATCTGAGGCGAATCTCAGTAGACAAAGCAACCCCTT 60

Qy 129 ACCGATTTTCGCTTCCCATTTATCTCTCCATTTATCTGCGAGCCCTTACCATAGTA 188
Db 61 ACCGATTTTCGCTTCCCATTTATCTCTCCATTTATCTCATTATCATCATAGCAATTTGCCATAGTC 120

Qy 189 CACCTACTGTTTCTCCAGAAACAGGATCCCAACACCCACAGGAACTCTCATCAGACGCA 248
Db 121 CACCTACTATTTCTCCAGAAACAGGATCCCAACACCCACAGGAAATTTCTCAGACGTA 180

Qy 249 GACAAAATTCATTTCCACCCCTACTACACTATCAAGATATCTTAGGAGCTCTACTATTA 308
Db 181 GACAAAATTCATTTCCACCCCTACTATACCATTAAGGACATCTTAGGGCCCTCTTACTA 240

Qy 309 ATTTTAACCCCTCATGCTTCTAGTCTATTTCTACCGGACCTGTTGGAGACCCAGACAAAC 368
Db 241 ATTCTAGCTCTTAATACTACTAGTACTATTTCGACCCGACCTCTCGGAGACCCAGATAAC 300

Qy 369 TATACACAGCAAAACCCACTTAATACACCCCCACATATCAAGCCCGAATGATCTTCTTA 428
Db 301 TACACCCGAGCAATCACTACACACACCCCTCATATCAAAACCCGAGTATCTTCTTA 360

Qy 429 TTTCATACGCAATCTCCGATCAATTTCTTAACAAACTAGGAGG 472
Db 361 TTTCATACGCAATCTTACGATCAATCCCAACAACTAGGAGG 404

RESULT 7
US-10-308-264-370
; Sequence 370, Application US/10308264
; Publication No. US20040029133A1
; GENERAL INFORMATION:
; APPLICANT: Herrnstadt, Corinna
; TITLE OF INVENTION: MITOCHONDRIAL DNA POLYMORPHISM
; FILE REFERENCE: 660088.461
; CURRENT APPLICATION NUMBER: US/10/308,264
; CURRENT FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 370
; LENGTH: 16565
; <211> conflict
; TYPE: DNA
; ORGANISM: Homo sapiens mitochondrial
; FEATURE:
; LOCATION: 3110
; OTHER INFORMATION: "n" refers to a nucleotide at position 3107 of the
; OTHER INFORMATION: Cambridge Reference Sequence (CRS, Anderson et al.
; OTHER INFORMATION: 1981 Nature 290:457-465), later determined to be
; OTHER INFORMATION: absent from the human mtDNA sequence according to
; OTHER INFORMATION: the revised CRS (rCRS, Andrews et al. 1999 Nature
; OTHER INFORMATION: Genetics 23:147); "n" therefore represents a
; OTHER INFORMATION: single nucleotide deletion at a position corresponding to
; OTHER INFORMATION: nucleotide 3107 of SEQ ID NO:1 as provided herein.
US-10-308-264-370

Query Match      61.0%; Score 288; DB 16; Length 16565;
Best Local Similarity 75.6%; Pred. No. 4.1e-79;
Matches 357; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

Qy 1 TACCATGAGGACAAATATCTTTTGGAGGACCAAGTCAATCACCATCTCTTTTCAGCAA 60
Db 15138 TCCGTGAGGCCAAATATCATTTCTGAGGGGCCACAGTAATTAACAATCTATCTATCCGCCA 15137

Qy 61 TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTCTCAGTAGATAAAG 120
Db 15198 TCCCATACATTTGGGACAGACCTAGTTCAATGAATCTGAGGAGGCTACTCAGTAGACAGTC 15257

Qy 121 CAACCCCTTACCCGATTTTTCGCTTCCACTTTATCTCTCCCATTTATCATATTGACGCCCTTA 180
Db 15258 CCACCCCTCACAGGATTTCTTTACCTTTCCTTCACTTCTTCTGCCCCTTCAATTATTGACGCCCTAG 15317

Qy 181 CCATAGTACACTACTGTTTCTCCAGAAACAGAGATCCAAACCCACAGGAATCTCAT 240
Db 15318 CAGCACTCCACCTCTTATTTCTTGACGAAACGGGATCAAAACCCCTTAGGAATCACT 15377

Qy 241 CAGACGAGACAAATTCATTTCCACCCCTACTACACTATCAAGATATCTTAGGAGCTC 300
Db 15378 CCCATTCCGACAAATTCATTTCCACCCCTACTACAGATCAAGATCAAGCCCTCGGCTTAC 15437

Qy 301 TACTATTAAATTTAAACCCCTCAATGCTTCTAGTCTTATCTACCGGACCTGCTTGGAGACC 360
Db 15438 TTCTCTTCTCTCTCTCTTAATGACATTAACACTATTCTCACCAGACCTCTAGGCGACC 15497

Qy 361 CAGCAACTATACACCGCAACCCACTTAATACACCCCCACATATCAAGCCCGAATGAT 420
Db 15498 CAGCAATATATACCTTAGCCAAACCCCTTAAATATCCCTTCCCATCAATCAAGCCCGAATGAT 15557

Qy 421 ACTTCTTATTTGCAATGAGCAATCTCCGATCAATTTCTTAAACAAACTAGGAGG 472
Db 15558 ATTCTCTATTTCGCTTACACAAATTTCCGATCCGCTCCCTTACAAACTAGGAGG 15609

RESULT 8
US-10-308-264-479
; Sequence 479, Application US/10308264
; Publication No. US20040029133A1
; GENERAL INFORMATION:
; APPLICANT: Herrnstadt, Corinna
; TITLE OF INVENTION: MITOCHONDRIAL DNA POLYMORPHISM
; FILE REFERENCE: 660088.461
; CURRENT APPLICATION NUMBER: US/10/308,264
; CURRENT FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 479
; LENGTH: 16569
; <211> conflict
; TYPE: DNA
; ORGANISM: Homo sapiens mitochondrial
; FEATURE:
; LOCATION: 3107
; OTHER INFORMATION: "n" refers to a nucleotide at position 3107 of the
; OTHER INFORMATION: Cambridge Reference Sequence (CRS, Anderson et al.
; OTHER INFORMATION: 1981 Nature 290:457-465), later determined to be
; OTHER INFORMATION: absent from the human mtDNA sequence according to
; OTHER INFORMATION: the revised CRS (rCRS, Andrews et al. 1999 Nature
; OTHER INFORMATION: Genetics 23:147); "n" therefore represents a
; OTHER INFORMATION: single nucleotide deletion at a position corresponding to
; OTHER INFORMATION: nucleotide 3107 of SEQ ID NO:1 as provided herein.
US-10-308-264-479

Query Match      61.0%; Score 288; DB 16; Length 16569;
Best Local Similarity 75.6%; Pred. No. 4.1e-79;
Matches 357; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

Qy 1 TACCATGAGGACAAATATCTTTTGGAGGACCAAGTCAATCACCATCTCTTTTCAGCAA 60
Db 15144 TCCGTGAGGCCAAATATCATTTCTGAGGGGCCACAGTAATTAACAATCTATCTATCCGCCA 15203

Qy 61 TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTCTCAGTAGATAAAG 120
Db 15198 TCCCATACATTTGGGACAGACCTAGTTCAATGAATCTGAGGAGGCTACTCAGTAGACAGTC 15257
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Db 15204 TCCATACATTGGGACAGACCTAGTTCAATGAATCTGAGGAGCTACTCAGTAGACAGTC 15263
QY 121 CAACCTTTACCGGATTTTTCGGCTTCCACCTTTATCTCTCCATTTATCATTTGAGCCCTTA 180
Db 15264 CCACCTCCACAGGATTTCTTACCTTTTCACTTCTTGCCTTTCATTTATGAGCCCTTAG 15323
QY 181 CCATAGTACACCTACTGTTTCTCCAGAAACAGGATCCAAACCCACAGGAATCTCAT 240
Db 15324 CAACACTCCACTCTCTTATTTCTTGCGAAACGGGATCAAAACCCCTTAGGATCACT 15383
QY 241 CAGAGCAGACAAAATTCACCTCCACCTTACTACACTATCAAAAGATATCTTAGGAGTC 300
Db 15384 CCCATTCOGATAAATCACTTCCACCTTACTACACAATCAAGAGCGCTCTGGCTTAC 15443
QY 301 TACTATTAAATTTTAAACCTTCACTCTTCTAGCTTCTTCTTCTCAGCGACCTGCTTGGAGAC 360
Db 15444 TTCTCTTCAATCTCTCTTAAATGACATTAACACTATTCTCACAGACCTCTTAGGCGAC 15503
QY 361 CAGACAACTATACACAGCAAAACCCACTTAATACACCCCAATATCAAGCCCGAATGAT 420
Db 15504 CAGACAAATATACCTTAGCAACCCCTTAAACACCCCTCCCAATCAAGCCCGAATGAT 15563
QY 421 ACTTCTTATTTGATACGCAATCTCCGATCAATCTTCACTTAACTAGGAGG 472
Db 15564 ATTCTCTATTCGCTACACAATCTCCGATCCGTCCTCCCTTAACTAGGAGG 15615

RESULT 9
US-10-308-264-213
; Sequence 213, Application US/10308264
; Publication No. US20040029133A1
; GENERAL INFORMATION:
; APPLICANT: HerinStadt, Corinna
; TITLE OF INVENTION: MITOCHONDRIAL DNA POLYMORPHISM
; FILE REFERENCE: 660088.461
; CURRENT APPLICATION NUMBER: US/10/308,264
; CURRENT FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 213
; LENGTH: 16570
; TYPE: DNA
; ORGANISM: Homo sapiens mitochondrial
; FEATURE:
; LOCATION: 3108
; OTHER INFORMATION: "n" refers to a nucleotide at position 3107 of the
; OTHER INFORMATION: Cambridge Reference Sequence (CRS, Anderson et al.
; OTHER INFORMATION: 1981 Nature 290:457-465), later determined to be
; OTHER INFORMATION: absent from the human mtDNA sequence according to
; OTHER INFORMATION: the revised CRS (rCRS, Andrews et al. 1999 Nature
; OTHER INFORMATION: Genetics 23:147); "n" therefore represents a
; OTHER INFORMATION: single nucleotide deletion at a position corresponding to
; OTHER INFORMATION: nucleotide 3107 of SEQ ID NO:1 as provided herein.
US-10-308-264-213

Query Match 61.0%; Score 288; DB 16; Length 16570;
Best Local Similarity 75.6%; Pred. No. 4.1e-79;
Matches 357; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCTTTTGGAGGACACAGTCATCACCAATCTCTTTACGAA 60
Db 15145 TCCCATGAGGCAAAATATCATCTTGAGGGGCCACAGTAATTAACAACTTACTATCCGCCA 15204
QY 61 TCCCATACATCGGTACAAACCTAGTAGAATCTGAGGAGGTTCTCAGTAGATAAAG 120
Db 15205 TCCCATATGTTGGACAGACCTAGTTCATGAACTGAGGAGGCTACTCAGTAGACAGTC 15264
QY 121 CAACCTTTACCGGATTTTTCGGCTTCCACCTTTATCTCTCCATTTATCATTTGAGCCCTTA 180
Db 15265 CCACCTCCACAGGATTTCTTACCTTTTCACTTCTTACCTTACCTTATTTGAGCCCTTAG 15324
QY 181 CCATAGTACACCTACTGTTTCTCCAGAAACAGGATCCAAACCCACAGGAATCTCAT 240
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Db 15325 CAGCACTCCACCTCTTATTTCTTGCGAAACAGGATCAAAACCCCTTAGGAATCACCT 15384
QY 241 CAGAGCAGACAAAATTCATTTCCACCCCTACTACACTATCAAGATATCTTAGGAGTC 300
Db 15385 CCCATTCOGATAAATCACTTCCACCTTACTACACAATCAAGAGCGCTCTGGCTTAC 15444
QY 301 TACTATTAAATTTTAAACCTTCACTCTTCTAGCTTCTTCTTCTCAGCGACCTGCTTGGAGAC 360
Db 15445 TTCTCTTCTCTCTCTTAAATGACATTAACACTATTCTCAGCTTCTTAGGCGAC 15504
QY 361 CAGACAACTATACACAGCAAAACCCACTTAAATACACCCCAATATCAAGCCCGAATGAT 420
Db 15505 CAGACAAATATACCTTAGCAACCCCTTAAACACCCCTCCCAATCAAGCCCGAATGAT 15564
QY 421 ACTTCTTATTTGATACGCAATCTCCGATCAATCTTCACTTAACTAGGAGG 472
Db 15565 ATTCTCTATTCGCTTACACAATCTCCGATCCGTCCTCCCTTAACTAGGAGG 15616

RESULT 10
US-10-308-264-287
; Sequence 287, Application US/10308264
; Publication No. US20040029133A1
; GENERAL INFORMATION:
; APPLICANT: HerinStadt, Corinna
; TITLE OF INVENTION: MITOCHONDRIAL DNA POLYMORPHISM
; FILE REFERENCE: 660088.461
; CURRENT APPLICATION NUMBER: US/10/308,264
; CURRENT FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 287
; LENGTH: 16572
; TYPE: DNA
; ORGANISM: Homo sapiens mitochondrial
; FEATURE:
; LOCATION: 3110
; OTHER INFORMATION: "n" refers to a nucleotide at position 3107 of the
; OTHER INFORMATION: Cambridge Reference Sequence (CRS, Anderson et al.
; OTHER INFORMATION: 1981 Nature 290:457-465), later determined to be
; OTHER INFORMATION: absent from the human mtDNA sequence according to
; OTHER INFORMATION: the revised CRS (rCRS, Andrews et al. 1999 Nature
; OTHER INFORMATION: Genetics 23:147); "n" therefore represents a
; OTHER INFORMATION: single nucleotide deletion at a position corresponding to
; OTHER INFORMATION: nucleotide 3107 of SEQ ID NO:1 as provided herein.
US-10-308-264-287

Query Match 61.0%; Score 288; DB 16; Length 16572;
Best Local Similarity 75.6%; Pred. No. 4.1e-79;
Matches 357; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCTTTTGGAGGACACAGTCATCACCAATCTCTTTACGAA 60
Db 15147 TCCCGTGAGGCCAAATATCATCTTGAGGGGCCACAGTAATTAACAACTTACTATCCGCCA 15206
QY 61 TCCCATACATCGGTACAAACCTAGTAGAATCTGAGGAGGTTCTCAGTAGATAAAG 120
Db 15207 TCCCATACATGTTGGACAGACCTAGTTCATGAACTGAGGAGGCTACTCAGTAGACAGTC 15266
QY 121 CAACCTTTACCGGATTTTTCGGCTTCCACCTTTATCTCTCCATTTATCATTTGAGCCCTTA 180
Db 15267 CCACCTTCACAGATTTCTTACCTTTTCACTTCTTACCTTATTTGAGCCCTTAG 15326
QY 181 CCATAGTACACCTACTGTTTCTCCAGAAACAGGATCCAAACCCACAGGAATCTCAT 240
Db 15327 CAACCTCCACCTCTCTGTTCTTGCGAAACGGGATCAAAACCCCTTAGGAATCACCT 15386
QY 241 CAGAGCAGACAAAATTCATTTCCACCCCTACTACACTATCAAGATATCTTAGGAGTC 300
Db 15387 CCCATTCOGATAAATCACTTCCACCTTACTACACAATCAAGAGCGCTCTGGCTTAC 15446
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RESULT 14


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; TYPE: DNA
; ORGANISM: Homo sapiens mitochondrial
; FEATURE:
; LOCATION: 3108
; OTHER INFORMATION: "n" refers to a nucleotide at position 3107 of the
; Cambridge Reference Sequence (CRS, Anderson et al.
; 1981 Nature 290:457-465), later determined to be
; OTHER INFORMATION: absent from the human mtDNA sequence according to
; the revised CRS (rCRS, Andrews et al. 1999 Nature
; Genetics 23:147); "n" therefore represents a
; OTHER INFORMATION: single nucleotide deletion at a position corresponding to
; nucleotide 3107 of SEQ ID NO:1 as provided herein.
US-10-308-264-206

Query Match          60.7%; Score 286.4; DB 16; Length 16561;
Best Local Similarity 75.4%; Pred. No. 1.3e-78;
Matches 356; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

Qy 1 TACCATGAGGCAAAATATCTTTTTCAGGAGCAACAGTCATCACCAATCTCCTTTTCAGCAA 60
Db 15136 TCCCGTGAGGCCAAATATCATCTCTGAGGGGCCACAGTAATTACAAACTTACTATCCGCCA 15195

Qy 61 TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTTCTCAGTAGATAAAG 120
Db 15196 TCCCATACATTTGGGACAGACCTAGTTCAATGAATCTGAGGAGGCTACTCAGTAGACAGTC 15255

Qy 121 CAAGCCCTTACCCGATTTTTCGCTTCCACTTTATCTCTCCCATTTATCATTTGCAGCCCTTA 180
Db 15256 CCACCCCTCAGAGATTCTTTACCTTCACTTCTGCCCCCTTATTTATTTGAGCCCTTAG 15315

Qy 181 CCATAGTACACTACTGTGTTCTCCAGAAACAGGATCCAAACCCCAACAGGAATCTCAT 240
Db 15316 CAGCACTCCACCTCCTATTCTTTGACGAAACGGGATCAACACCCCTAGGAATCACCT 15375

Qy 241 CAGAGCGACAGAAATTCCTATTCACCCCTACTACATATCAAAAGATATCCTAGGAGCTC 300
Db 15376 CCCATTCCGATAAAATCACTTCCACCCCTTACTACAAATCAAAAGAGCCCTCGGCTTAC 15435

Qy 301 TACTATTAAATTTAACCCCTCATGCTTCTAGTCTTATTTCTACCGGACCTGCTTGGAGACC 360
Db 15436 TTCTCTTCCCTTCTCTCCTTAATGACATTAACACTATTTCTACAGACCTCTTAGGGACC 15495

Qy 361 CAGCAACTATACACCGAAACCCACTTAATACACCCCAATATCAAGCCCGAATGAT 420
Db 15496 CAGCAAAATTAACCTAGCCCAACCCCTAAATACCCCTCCCAATCAAGCCCGAATGAT 15555

Qy 421 ACTTCCCTATTTGCATACCGAATCTCCGATCAATTCCTAACAACTAGGAGG 472
Db 15556 ATTTCCCTATTCGCTACACAAATCTCCGATCCGTCCTCAACAACTAGGAGG 15607
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Search completed: November 17, 2004, 03:11:54
Job time : 706.939 secs

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Db	398	TACCATTGAGGACAAATATCTTTTTGAGGAGCAACAGTCATCACCAATCTCCTTTTCAGCAA	457			
Qy	61	TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTTCTCAGTAGATAAAG	120			
Db	458	TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTTCTCAGTAGATAAAG	517			
Qy	121	CAACCCCTTACCCGATTTTTTCGGCTTCCACTTTATCCTCCCATTTATCATTCGACGCCCTTA	180			
Db	518	CAACCCCTTACCCGATTTTTTCGGCTTCCACTTTATCCTCCCATTTATCATTCGACGCCCTTA	577			
Qy	181	CGATAGTACACCTACTGTTTCTCCAGAAACAGGATCCAAACCCCAAGGAATCTTCAT	240			
Db	578	CGATAGTACACCTACTGTTTCTCCAGAAACAGGATCCAAACCCCAAGGAATCTTCAT	637			
Qy	241	CAGACGCGACAAAAATTCOATTCACCCCTTACTACACTATCAAAGATATCCTTAGGAGCTC	300			
Db	638	CAGACGCGACAAAAATTCOATTCACCCCTTACTACACTATCAAAGATATCCTTAGGAGCTC	697			
Qy	301	TACTATTATTTTAAACCTCATGCTTCTAGTCTCTATTTCTCACCGGACCTGTTGGAGACC	360			
Db	698	TACTATTATTTTAAACCTCATGCTTCTAGTCTCTATTTCTCACCGGACCTGTTGGAGACC	757			
Qy	361	CAGACAACATATACCCAGCAAAACCCACTTAAATACACCCCAATATCAAGCCCGGAATGAT	420			
Db	758	CAGACAACATATACCCAGCAAAACCCACTTAAATACACCCCAATATCAAGCCCGGAATGAT	817			
Qy	421	ACTTCTATTTTGATACGGCAATCCTCCGATCAATTCCTTAACAACTAGGAGG	472			
Db	818	ACTTCTATTTTGATACGGCAATCCTCCGATCAATTCCTTAACAACTAGGAGG	869			

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RESULT 3
AF036283
LOCUS          linear   MM 01-DEC-1999
DEFINITION    Antelope cervicapra cytochrome b (cytb) gene, mitochondrial gene
               encoding mitochondrial protein, partial cds.
ACCESSION     AF036283
VERSION       AF036283.1 GI:5777927
KEYWORDS
SOURCE        mitochondrion Antelope cervicapra (blackbuck)
ORGANISM      Antelope cervicapra
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
               Antilopinae; Antelope.
REFERENCE     1 (bases 1 to 1139)
               Hassanin,A. and Douzery,E.J.
               The tribal radiation of the family Bovidae (Artiodactyla) and the
               evolution of the mitochondrial cytochrome b gene
               Mol. Phylogenet. Evol. 13 (2), 227-243 (1999)
JOURNAL       20072924
MEDLINE       10603253
PUBMED
REFERENCE     2 (bases 1 to 1139)
               Hassanin,A.
               Direct Submission
               Submitted (02-DEC-1997) Systematique Moleculaire (GDR 1005), Museum
               National d'Histoire Naturelle, 43, rue Cuvier, Paris 75005, France
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    CDS

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Query Match	100.0%;	Score 472;	DB 4;	Length 1140;
Best Local Similarity	100.0%;	Pred. No. 1.4e-124;		

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OM nucleic - nucleic search, using sw model

Run on: November 16, 2004, 22:24:28 ; Search time 6487.97 Seconds
(without alignments)
2650.992 Million cell updates/sec

Title: US-09-821-782E-48
Perfect score: 472
Sequence: 1 taccatgggacaaatatct.....attcctaacaactaggagg 472

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_hic:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gss1:*
- 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	368	78.0	803	7	CN822665 Oa splbn
2	362.2	76.7	670	7	CF614528 CES008735
3	362	76.7	840	7	CN822842 Oa splbn
4	361.6	76.6	571	4	BG689885 338199 BA
5	361.6	76.6	574	6	CB220822 1AB026G11
6	361.6	76.6	692	6	CB449349 703541 MA
7	361.6	76.6	727	6	CB444500 695671 MA
8	361.6	76.6	728	6	CB439091 688000 MA
9	359	76.1	863	7	CN824188 Oa splbn
10	355.6	75.3	515	6	CB223436 1JEJ23E10
11	355.6	75.3	552	6	CB220605 1AB024C06
12	355.6	75.3	735	7	CR451416 CR451416
13	355	75.2	648	7	CN789904 4124424 B
14	354.6	75.1	560	4	BM433529 1Ru5B7.a
15	353.6	74.9	487	4	BM434623 1R11A03
16	352.6	74.7	848	7	CN822875 Oa splbn
17	351	74.4	610	6	CB537456 775083 MA
18	350.6	74.3	575	2	BB590256 197290 BA
19	350.6	74.3	664	1	AV610345 AV610345
20	350.6	74.3	670	6	CB449447 703648 MA
21	350	74.2	462	6	CB536710 771751 MA
22	350	74.2	729	6	CB454877 711703 MA
23	344.6	73.0	481	4	BM434031 1R701B01
24	343.2	72.7	536	6	CB226776 1Ru30A04

25	335.8	71.1	566	6	CB223865	CB223865	1JEB28F7	
26	334.8	70.9	534	6	CB223377	CB223377	1JEB22H10	
27	332.8	70.5	674	7	CN003741	CN003741	IP38C05.9	
28	332.8	70.5	874	7	CK462186	CK462186	932968 MA	
C	29	332.8	70.5	926	7	CK998194	IP28F03.b	
30	331.2	70.2	541	5	BX918855	BX918855	EX918855	
31	331.2	70.2	755	7	CK462843	CK462843	933666 MA	
32	331.2	70.2	823	7	CK461830	CK461830	932584 MA	
33	331.2	70.2	830	7	CN155599	CN155599	942910 MA	
34	331.2	70.2	880	7	CN003411	CN003411	IP16G03.g	
35	331.2	70.2	887	7	CK454695	CK454695	915197 MA	
C	36	329.6	69.8	1277	7	AV665191	AV665191	
37	329.6	69.8	436	4	BM434645	BM434645	1RT11C06	
38	328.8	69.7	629	7	CF615029	CF615029	CES008505	
39	328.8	69.7	629	7	BP110912	BP110912	BP110912	
40	326.6	69.2	764	4	BI817190	BI817190	IBt222 Swi	
41	326.4	69.2	764	4	CB447959	CB447959	702011 MA	
C	42	326.2	69.1	705	6	CK462480	CK462480	933282 MA
43	324	68.6	748	7	BF450916	BF450916	uz72d11.y	
C	44	323.2	68.5	679	2	CB573135	AGENCOURT	
45	323.2	68.5	748	6	CB573135	CB573135	UZ72D11.Y	

ALIGNMENTS

RESULT 1
CN822665
LOCUS
DEFINITION
Oa_splbn_02017_M13reverse Sheep spleen/brain pSport1 library Ovis aries cDNA clone Oa_splbn_02017 5', mRNA sequence.
803 bp mRNA linear EST 02-JUN-2004
ACCESSION
CN822665
VERSION
CN822665.1
KEYWORDS
EST.
SOURCE
Ovis aries (sheep)
ORGANISM
Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Caprinae; Ovis.
REFERENCE
1 (bases 1 to 803)
Gossner,A. and Hopkins,J.
Ovine spleen/brain cdna library
TITLE
Unpublished (2004)
JOURNAL
COMMENT
Contact: J Hopkins
Veterinary Biomedical Sciences
University of Edinburgh
Summerhall Square, Edinburgh, EH9 1QH.
Email: j.hopkins@ed.ac.uk
Plate: 02 row: O column: 17
Seq primer: M13reverse
High quality sequence start: 6
High quality sequence stop: 549.
FEATURES
source
Location/Qualifiers
1..803
/organism="Ovis aries"
/mol_type="mRNA"
/db_xref="taxon:9940"
/clone="Oa_splbn_02017"
/library="Sheep spleen/brain pSport1 library"

ORIGIN
Query Match 78.0%; Score 368; DB 7; Length 803;
Best Local Similarity 86.2%; Pred. No. 4e-97;
Matches 407; Conservative 0; Mismatches 65; Indels 0; Gaps 0;
Qy 1 TACCATGAGCAAAATATCTTTTGAGGACAAACAGTCATCACAAATCTCTTCAGCAA 60
Db 87 TACCATGAGCAAAATATCTTTTGAGGACAAACAGTCATCACAAATCTCTTCAGCAA 146
Qy 61 TCCATATCGGTACAACTAGTAGAATCTCAGGAGGTTCTCAGTAGATAAAG 120
Db 147 TTCCATATATTGGCACAAACCTAGTCGATGAATCTGGGAGGATTCTCAGTAGACAAG 206

QY 121 CAACCTTTACCGATTTTTCGCTTCCACTTATCTCCATTTATCATTCGAGCCCTTA 180
 Db 207 CTACCTCAGCGGATTTTTCGCTTTCCTTCACTTTATTTTCCATTCATCGAGCCCTCG 266
 QY 181 CCATAGTACACTTACTGTTTCTCCAGAAACAGGATCCAAACCCACAGGAATCTCAT 240
 Db 267 CCATAGTTCACCTACTCTCTCTCCAGAAACAGGATCCAAACCCACAGGAATTCAT 326
 QY 241 CAGACGAGACAAATTCATTCACCCCTTACTACTACTATCAAGATATCTAGAGCTC 300
 Db 327 CGGACACAGATAAATTCCTTCCACCTTATTAACACATTAAGACATCTTAGTGCTA 386
 QY 301 TACTATTATTTAAACCTTCATGCTTCTAGTCTCTTCTCAGGACCTGCTTGAGACC 360
 Db 387 TCCTACTAATCTCATCTCTGCTACTAGTACTTATTCAGGCTGACTTACTTCGAGACC 446
 QY 361 CAGACAACTATACACAGAAACCCACTTAATATACACCCGACATATCAAGCCCGAATGAT 420
 Db 447 CAGACAACTATACACCCGAAACCCACTTAATATACACCTCCGCTCACAATCAACCTGAATGAT 506
 QY 421 ACTTCCTATTGATACGCAATCTCCGATCAATTCCTAAACAACTAGGAGG 472
 Db 507 ACTTCCTATTGCTGACGCAATCTTACGATCAATCCCTAAATAACTAGGAGG 558

RESULT 2
 LOCUS CF614528 670 bp mRNA linear EST 01-OCT-2003
 DEFINITION CES008735 Bos taurus muscle cDNA library Bos taurus cDNA clone
 CF614528
 VERSION CF614528
 KEYWORDS EST.
 SOURCE Bos taurus (cow)

ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.
 REFERENCE 1 (bases 1 to 670)
 AUTHORS Wang, Y.H., Byrne, K., Vuocolo, T., Tan, S.H., McWilliam, S., Dierens, L.
 and Lehnert, S.
 TITLE Transcription profiling of bovine skeletal muscle and subcutaneous
 fat

JOURNAL Unpublished (2003)
 COMMENT Contact: Dr Sigrud Lehnert
 Functional Genomics Lab
 CSIRO Livestock Industries
 Level 5, Queensland Bioscience Precinct, University of Queensland,
 306 Carmody Road St. Lucia QLD Australia
 Tel: 07 3214 2445
 Fax: 07 3214 2480
 Email: Sigrud.Lehnert@csiro.au
 Plate: 11 row: C column: 03.

FEATURES
 source
 1. .670
 /organism="Bos taurus"
 /mol_type="mRNA"
 /strain="Angus"
 /db_xref="taxon:9913"
 /clone="CCL008735"
 /sex="male"
 /tissue_type="Longissimus dorsi muscle"
 /dev_stage="Young Adult"
 /lab_host="XLI-BlueMRF'strain"
 /clone_lib="Bos taurus muscle cDNA library"
 /note="Organ: skeletal muscle; Vector: Uni-ZAPXR; Site 1:
 EcoRI; Site 2: Xho I; Library made from skeletal muscle of
 a 14 month old Angus steer."

ORIGIN

Query Match 76.7%; Score 362.2; DB 7; Length 670;
 Best Local Similarity 85.4%; Pred. No. 1.9e-95;
 Matches 403; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 1 TACCATGAGGACAAATATCTTTTTCAGGAGCAAGTATCACCATCTCCTTTTCAGGAA 60
 Db 33 TACCATGAGGACAAATATCTTTTTCAGGAGCAAGTATCACCATCTCCTTTTCAGGAA 92
 QY 61 TCCCATATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGTTCTCAGTAGATAAG 120
 Db 93 TCCCATATCGGACAAATTTAGTCGAATGAATCTGAGGCGGATCTCAGTAGACAAAG 152
 QY 121 CAACCTTTACCGATTTTTCGCTTTCCTTATCTCCCTTATCTATTCAGGCCCTTA 180
 Db 153 CAACCTTTACCGATTTTTCGCTTTCCTTATCTCCCTTATCTATTCAGGCAATTTG 212
 QY 181 CCATAGTACACTTACTGTTTCTCCAGAAACAGGATCCAAACCCACAGGAATCTCAT 240
 Db 213 CCATAGTCCACTTACTTCTCTCCAGAAACAGGCTCCAAACCCACAGGAATTTCT 272
 QY 241 CAGACGAGACAAATTCATTCACCCCTTACTACTATCAAGATATCTTAGGAGCTC 300
 Db 273 CAGACGTAGACAAATTCCTTCCACCTTACTATACCATTAAGGACATCTTAGGAGCCC 332
 QY 301 TACTATTATTTTAAACCTCATGCTTCTAGTCTCTTATCTCAGGACCTGCTTGAGACC 360
 Db 333 TCTTACTAATTTCTAGCTCTAATCTACTAGTACTTTCGACCCGACCTCTCTCGGAGACC 392
 QY 361 CAGACAACTATACACCGAAACCCACTTAATATACACCCGACATATCAAGCCCGAATGAT 420
 Db 393 CAGATAACTACACCCGAGCAATCACTCAACACACACCCCTCACAATCAACCCGAGTAT 452
 QY 421 ACTTCCTATTGCTAGGCAATCTCCGATCAATTCCTTAACAACTAGGAGG 472
 Db 453 ACTTCCTATTGCTAGGCAATCTTACGATCAATCCCTCAACAACTAGGAGG 504

RESULT 3

LOCUS

DEFINITION

840 bp mRNA linear EST 02-JUN-2004
 Oa splbn_02G06_M13reverse Sheep spleen/brain pSport1 library Ovis
 aries cDNA clone Oa_splbn_02G06 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT

UNPUBLISHED

CONTACT

FUNCTIONAL

GENOMICS

LAB

LEVEL

UNIVERSITY

OF

QUEENSLAND,

306

CARMODY

ROAD

ST. LUCIA

QLD

AUSTRALIA

TEL:

07 3214 2445

FAX:

07 3214 2480

EMAIL:

Sigrud.Lehnert@csiro.au

PLATE:

11 row: C column: 03.

LOCATION/QUALIFIERS

1. .840

/organism="Ovis aries"

/mol_type="mRNA"

/db_xref="taxon:9940"

/clone="Oa splbn_02G06"

/clone_lib="Sheep spleen/brain pSport1 library"

ORIGIN

Query Match 76.7%; Score 362; DB 7; Length 840;

Best Local Similarity 86.1%; Pred. No. 2.3e-95;

Matches 401; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

FEATURES
source

Location/Qualifiers
1. .574
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="Smooth muscle"
/cell_type="Epithelial"
/dev_stage="Young adult"
/lab_host="XLI-BlueMRF'-strain"
/clone_lib="Bos taurus Abomasum #1 library"
/note="Organ: Abomasum; Vector: Uni-ZAPRR; Site 1: EcoR
I; Site 2: Xho I"

ORIGIN

Query Match 76.6%; Score 361.6; DB 6; Length 574;
Best Local Similarity 85.4%; Pred. No. 2.8e-95;
Matches 403; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

Qy 1 TACCATGAGGACAAATATCTTTTGGAGGACCAAGTCATCACCAGTCTCTCTTTTCAGCAA 60
Db 21 TACCATGAGGACAAATATCAATCTGAGGACCAAGTCATCACCAGTCTCTCTTTTCAGCAA 80
Qy 61 TCCCATACATCGGTACCAACTAGTGAATGAATCTGAGGAGGTTCTCAGTAGATAAAG 120
Db 81 TCCCATACATCGGCACAAATTTAGTCGAATGAATCTGAGGAGGTTCTCAGTAGATAAAG 140
Qy 121 CAACCCCTTACCCGATTTTTCGCTTCCACTTTATCTCTCCCTTTATCATTCAGGCCCTTA 180
Db 141 CAACCCCTTACCCGATTTTTCGCTTCCACTTTATCTCTCCCTTTATCATTCAGGCAATG 200
Qy 181 CCATAGTACACTACTGTTTCTCCAGGAAACAGGATCCAAACCCACAGGAATCTCAT 240
Db 201 CCATAGTCCACTACTATTTCTCCAGGAAACAGGATCCAAACCCACAGGAATTTTCT 260
Qy 241 CAGAGGAGACAAATTCATTCACCCCTTACTACACTATCAAGATATCTTAGAGGTC 300
Db 261 CAGAGGAGACAAATTCATTCACCCCTTACTACACTATCAAGATATCTTAGAGGTC 320
Qy 301 TACTATTAATTTTAAACCTCTAGTCTTCTAGTCTTATCTCACCAGGCTCTTGGAGACC 360
Db 321 TCTTACTAATTTTAAACCTCTAGTCTTATCTAGTCTTATCTCACCAGGCTCTTGGAGACC 380
Qy 361 CAGACACTATACACGAGCAACCACTTAATACACCCCAATATCAAGCCCAATGAT 420
Db 381 CAGATAACTACACCCAGCAATCCACTCAACACACCCCTTCAATCAACCCAGTGAT 440
Qy 421 ACTTCTTATTTGCATAGCAATCTCTCCGATCAATTCCTTAACAACTAGGAG 472
Db 441 ACTTCTTATTTGCATAGCAATCTTACGATCAATTCCTTAACAACTAGGAG 492

RESULT 6

CB449349 692 bp mRNA linear EST 26-MAR-2003
LOCUS
DEFINITION 703541 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION CB449349
VERSION
KEYWORDS EST.
SOURCE
ORGANISM Bos taurus (cow)

REFERENCE

AUTHORS Smith, T.P.L., Roberts, A.J., Echtenkamp, S.E., Chitko-McKown, C.G., Wray, J.E. and Keele, J.W.
TITLE A second set of bovine ESTs from pooled-tissue normalized libraries
JOURNAL Unpublished (2003)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390

Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329.
Plate: FQY8059 row: L column: 22
Seq primer: GTAATACGACTCACTATAGG.
Location/Qualifiers
1. .692

FEATURES

source
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 6BOV"
/note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."

ORIGIN

Query Match 76.6%; Score 361.6; DB 6; Length 692;
Best Local Similarity 85.4%; Pred. No. 2.9e-95;
Matches 403; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

Qy 1 TACCATGAGGACAAATATCTTTTGGAGGACCAAGTCATCACCAGTCTCTCTTTTCAGCAA 60
Db 16 TACCATGAGGACAAATATCAATCTGAGGAGCAAGTCATCACCAGTCTCTCTTTTCAGCAA 75
Qy 61 TCCCATACATCGGTACCAACCTAGTGAATGAATCTGAGGAGGTTCTCAGTAGATAAAG 120
Db 76 TCCCATACATCGGCACAAATTTAGTCGAATGAATCTGAGGAGGTTCTCAGTAGATAAAG 135
Qy 121 CAACCCCTTACCCGATTTTTCGCTTCCACTTTATCTCTCCCTTTATCATTCAGGCCCTTA 180
Db 136 CAACCCCTTACCCGATTTTTCGCTTCCACTTTATCTCTCCCTTTATCATTCAGCAATG 195
Qy 181 CCATAGTACACTACTGTTTCTCCAGGAAACAGGATCCAAACCCACAGGAATCTCAT 240
Db 196 CCATAGTCCACTACTATTTCTCCAGGAAACAGGATCCAAACCCACAGGAATTTCT 255
Qy 241 CAGAGGAGACAAATTTCCATTCACCCCTTACTACACTATCAAGATATCTTAGAGGTC 300
Db 256 CAGAGGAGACAAATTTCCATTCACCCCTTACTACACTATCAAGATATCTTAGAGGTC 315
Qy 301 TACTATTAATTTTAAACCTCTAGTCTTCTAGTCTTATCTCACCAGGCTCTTGGAGACC 360
Db 316 TCTTACTAATTTTAAACCTCTAGTCTTATCTAGTCTTATCTCACCAGGCTCTTGGAGACC 375
Qy 361 CAGACACTATACACGAGCAACCCACTTAATACACCCCAATATCAAGCCCAATGAT 420
Db 376 CAGATAACTACACCCAGCAATCCACTCAACACACCCCTTCAATCAACCCAGTGAT 435
Qy 421 ACTTCTTATTTGCATAGCAATCTCTCCGATCAATTCCTTAACAACTAGGAG 472
Db 436 ACTTCTTATTTGCATAGCAATCTTACGATCAATTCCTTAACAACTAGGAG 487

RESULT 7

CB444500 727 bp mRNA linear EST 25-MAR-2003
LOCUS
DEFINITION 695671 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION CB444500
VERSION
KEYWORDS EST.
SOURCE
ORGANISM Bos taurus (cow)

REFERENCE

AUTHORS Smith, T.P.L., Roberts, A.J., Echtenkamp, S.E., Chitko-McKown, C.G., Wray, J.E. and Keele, J.W.
TITLE A second set of bovine ESTs from pooled-tissue normalized libraries

JOURNAL Unpublished (2003)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: FQY8052 row: H column: 9
Seq primer: GTAATACGACTCACTATAGG.
Location/Qualifiers
1. .727

FEATURES

source
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 6BOV"
/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."

ORIGIN

Query Match 76.6%; Score 361.6; DB 6; Length 727;
Best Local Similarity 85.4%; Pred. No. 3e-95;
Matches 403; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
QY 1 TACCATGAGGACAAATATCTTTTGGAGGACACAGTCATCACAATCTCTTCAGCAA 60
Db 60 TACCATGAGGACAAATATCTTTTGGAGGACACAGTCATCACAATCTCTTCAGCAA 119
QY 61 TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGTTCTCAGTAGATAAAG 120
Db 120 TCCCATACATCGGTACAAATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAG 179
QY 121 CAACCTTACCCGATTTTTCGCTTCCACATTTATCTCCCATTTATCATTTGACGCCCTTA 180
Db 180 CAACCTTACCCGATTTTTCGCTTCCATTTTATCTCTTCCATTTATCATATAGCAATTG 239
QY 181 CCATAGTACACCTACTGTTTCTCCAGAAACAGATCCCAACCCACACAGGAATCTCAT 240
Db 240 CCATAGTACACCTACTGTTTCTCCAGAAACAGATCCCAACCCACACAGGAATTTCTT 299
QY 241 CAGACGAGACAAATTCATTCACCCCTACTACATATCAAGATATCTTAGGAGCTC 300
Db 300 CAGACGTAGACAAATTCCTATTCACCCCTACTATACATTAAGGACATCTTAGGGGCC 359
QY 301 TACTATTAATTTAAACCTCATGCTTCTAGTCTTAATTTCTACCGGACCTCTGTGGAGACC 360
Db 360 TCTTACTAATTTAGCTCTAATACTACTAGTACTAATTTCTGACCCGACCTCTCTGGAGACC 419
QY 361 CAGACACTATACACGAGAAACCACTTAATACACCCCAATATCAAGCCGAATGAT 420
Db 420 CAGATAACTACACCCGAGCAATCCATCTACACACCCCTCATCAAAACCCGAGTAT 479
QY 421 ACTTCTTATTGGATAGCAATCTCCGATCAATTTCTTAACAACTAGGAGG 472
Db 480 ACTTCTTATTGGATAGCAATCTTAGATCAATCCCCACAACTAGGAGG 531

RESULT 8
LOCUS CB439091 728 bp mRNA linear EST 25-MAR-2003
DEFINITION 680000 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION CB439091
VERSION CB439091.1 GI:29223751
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
1 (bases 1 to 728)
Smith,T.P.L., Roberts,A.J., Echternkamp,S.E., Chitko-McKown,C.G.,
Wray,J.E. and Keele,J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries
Unpublished (2003)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross_match v0.990329.
Plate: FQY8044 row: L column: 23
Seq primer: GTAATACGACTCACTATAGG.
Location/Qualifiers
1. .728

FEATURES

source
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 6BOV"
/note="Vector: pcDNA3.1; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."

ORIGIN

Query Match 76.6%; Score 361.6; DB 6; Length 728;
Best Local Similarity 85.4%; Pred. No. 3e-95;
Matches 403; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
QY 1 TACCATGAGGACAAATATCTTTTGGAGGACACAGTCATCACAATCTCTTCAGCAA 60
Db 44 TACCATGAGGACAAATATCTTTTGGAGGACACAGTCATCACAATCTCTTCAGCAA 103
QY 61 TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGTTCTCAGTAGATAAAG 120
Db 104 TCCCATACATCGGTACAAATTTAGTCGAATGAATCTGAGGCGGATTCTCAGTAGACAAAG 163
QY 121 CAACCTTACCCGATTTTTCGCTTCCACATTTATCTCCCATTTATCATTTGACGCCCTTA 180
Db 164 CAACCTTACCCGATTTTTCGCTTCCATTTTATCTCTTCCATTTATCATATAGCAATTG 223
QY 181 CCATAGTACACCTACTGTTTCTCCAGAAACAGGATCCAAACCCCAAGGAATCTCAT 240
Db 224 CCATAGTACACCTACTGTTTCTCCAGAAACAGGATCCAAACCCCAAGGAATTTCTT 283
QY 241 CAGACGAGACAAATTCATTCACCCCTACTACATATCAAGATATCTTAGGAGCTC 300
Db 284 CAGACGTAGACAAATTCCTATTCACCCCTACTATACCATTAAGGACATCTTAGGGGCC 343
QY 301 TACTATTAATTTAAACCTCATGCTTCTAGTCTTAATTTCTACCGGACCTCTGTGGAGACC 360
Db 344 TCTTACTAATTTAGCTCTAATACTACTAGTACTAATTTCTGACCCGACCTCTCTGGAGACC 403
QY 361 CAGACACTATACACGAGAAACCCCACTTAATACACCCCAATATCAAGCCGAATGAT 420
Db 404 CAGATAACTACACCCGAGCAATCCATCTACACACCCCTCATCAAAACCCGAGTAT 463
QY 421 ACTTCTTATTGGATAGCAATCTCCGATCAATTTCTTAACAACTAGGAGG 472
Db 464 ACTTCTTATTGGATAGCAATCTTAGATCAATCCCCACAACTAGGAGG 515

RESULT 9
LOCUS CN824188 863 bp mRNA linear EST 02-JUN-2004
DEFINITION Oa_splbn_07C24_M13reverse Sheep spleen\brain pSport1 library Ovis

aries cDNA clone Oa_sp1bn_07C24 5', mRNA sequence.
 ACCESSION CN824188
 VERSION CN824188.1 GI:47952257
 KEYWORDS EST.
 SOURCE Ovis aries (sheep)
 ORGANISM Ovis aries

REFERENCE 1 (bases 1 to 863)
 AUTHORS Gosner, A. and Hopkins, J.
 TITLE Ovine spleen/brain cDNA library
 JOURNAL Unpublished (2004)
 COMMENT Veterinary Biomedical Sciences
 University of Edinburgh
 Summerhall Square, Edinburgh, EH9 1QH.
 Email: j.hopkins@ed.ac.uk
 Plate: 07 row: C column: 24
 Seq primer: M13reverse
 High quality sequence start: 6
 High quality sequence stop: 550.

FEATURES
 Location/Qualifiers
 1..863
 /organism="Ovis aries"
 /mol_type="mRNA"
 /db_xref="taxon:9940"
 /clone="Oa_sp1bn_07C24"
 /clone_lib="Sheep spleen/brain pSport1 library"

ORIGIN

Query Match 76.1%; Score 359; DB 7; Length 863;
 Best Local Similarity 86.0%; Pred. No. 1.8e-94;
 Matches 398; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

Oy 1 TACCATGAGGACAAATATCTTTTGGAGGACAAAGTCATCACCAATCTCTTTTCAGCAA 60
 Db |||||
 Oy 401 TACCATGAGGACAAATATCTTTGAGGAGCAACAGTCATCACCAATCTCTTTTCAGCAA 460
 Db |||||
 Oy 61 TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTCTCTCAGTAGATAAG 120
 Db |||||
 Oy 461 TTCCATATTTGGACAAACCTAGTCGAATGAATCTGGGAGGATTCAGTAGACAAAG 520
 Db |||||
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 Oy 521 CTAGCCTCACCGATTTTTCGCTTCCACGAAACAGGATCCAAACCCACAGGATCTTCA 580
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 Oy 181 CCATAGTACACTACTGTTTTCGCTTCCACGAAACAGGATCCAAACCCACAGGATCTTCA 240
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 Oy 581 CCATAGTACACTACTGTTTTCGCTTCCACGAAACAGGATCCAAACCCACAGGATCTTCA 640
 Db |||||
 Oy 241 CAGACGACAGCAAAATTCATTTCCACCCCTACTACTATCAAGATATCTTAGAGGATC 300
 Db |||||
 Oy 641 CGGACACAGATAAATTCCTTCCACCCCTACTACTATCAAGATATCTTAGAGGATC 700
 Db |||||
 Oy 301 TACTATTAATTTAAACCTCATGCTTCTAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 360
 Db |||||
 Oy 701 TCCTTAATCTCTCATCT 760
 Db |||||
 Oy 361 CAGACACTATACACGACCAACCCACTTAATACACCCCAATATCAAGCCCAATGAT 420
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 Oy 761 CAGCAACTACACCCCAAGCAACCCACTTAATACACCCCAATATCAAGCCCAATGAT 820
 Db |||||
 Oy 421 ACTTCTTATTTGCATAGGCAATCTCCGATCAATTTCTTAACA 463
 Db |||||
 Oy 821 ACTTCTTATTTGCATAGGCAATCTTAGATCAATTTCTTAACA 863
 Db |||||

RESULT 10
 CB223436
 LOCUS
 DEFINITION lJEJ23E10 Bos taurus Jejunum #1 library Bos taurus cDNA, mRNA
 sequence.
 515 bp mRNA linear EST 10-FEB-2003

ACCESSION CB223436
 VERSION CB223436.1 GI:28293950
 KEYWORDS EST.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus

REFERENCE 1 (bases 1 to 515)
 AUTHORS Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Senses, C.W.,
 Gordon, P.M.K. and Moore, S.S.
 TITLE Gene Expression Profiling of the Bovine Gastrointestinal Tract
 JOURNAL Unpublished (2002)
 COMMENT Contact: Dr. Stephen Moore
 Beef Genomics Laboratory
 Dept of AFNS, University of Alberta
 410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
 Tel: 780 492 0169
 Fax: 780 492 4265
 Email: stephen.moore@ualberta.ca
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FEATURES
 Location/Qualifiers
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 /clone_lib="Bos taurus Jejunum #1 library"
 /note="Organ: Intestine/Jejunum; Vector: Uni-2ZAPXR;
 Site_1: EcoRI; Site_2: Xho I"

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 Best Local Similarity 85.2%; Pred. No. 1.6e-93;
 Matches 397; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

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 Oy 61 TCCCATACATCGGTACAAACCTAGTAGAATGAATCTGAGGAGGGTCTCTCAGTAGATAAG 120
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 Oy 110 TCCCATACATCGGCACAAATTTAGTGAATGAATCTGAGCGGATTTCTCAGTAGACAAAG 169
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 Oy 170 CAACCTTACCCGATTTTTCGCTTCCATTTATCTCTTCCATTTATCATTCAGCAATG 229
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 Oy 181 CCATAGTACACTACTGTTTTCGCTTCCAGAAACAGGATCCAAACCCACAGGATCTCAT 240
 Db |||||
 Oy 230 CCATAGTCCACTACTATTTCTCCAGAAACAGGATCCAAACCCACAGGATTTCTCT 289
 Db |||||
 Oy 241 CAGACGACAGCAAAATTCATTTCCACCCCTACTACTATCAAGATATCTTAGAGGATC 300
 Db |||||
 Oy 290 CAGACGACAGCAAAATTCATTTCCACCCCTACTACTATCAAGATATCTTAGAGGATC 349
 Db |||||
 Oy 301 TACTATTAATTTAAACCTCATGCTTCTAGTCTTATTTCTCAGCGAGCTGCTTGGAGACC 360
 Db |||||
 Oy 350 TCCTTACTAATTTAGTCTTAATCTACTACTACTACTACTACTACTACTACTACTACTACT 409
 Db |||||
 Oy 361 CAGACAACTATACACGACAAACCCACTTAATACACCCCAATATCAAGCCCAATGAT 420
 Db |||||
 Oy 410 CAGATTAATACACCCCAAGCAATCTCAACACACCCCTCATCAACACCCGAGTAT 469
 Db |||||
 Oy 421 ACTTCTTATTTGCATAGGCAATCTCCGATCAATTTCTTAACA 466
 Db |||||
 Oy 470 ACTTCTTATTTGCATAGGCAATCTTAGATCAATTTCTTAACA 515
 Db |||||


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RESULT 11
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LOCUS      1Ab024C06 Bos taurus Abomasum #1 library Bos taurus cDNA, mRNA
DEFINITION
ACCESSION  CB220605
VERSION     CB220605
KEYWORDS   EST.
SOURCE      Bos taurus (cow)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE   1 (bases 1 to 552)
AUTHORS     Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., SENSEN, C.W.,
Gordon, P.M.K. and Moore, S.S.
TITLE       Gene Expression Profiling of the Bovine Gastrointestinal Tract
JOURNAL     Unpublished (2002)
COMMENT     Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
Tel: 780 492 0169
Fax: 780 492 4265
Email: stephen.moore@ualberta.ca
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FEATURES             Location/Qualifiers
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Best Local Similarity 85.2%; Pred. No. 1.6e-93;
Matches 397; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

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QY      61  TCCATACATCGGTACAACTAGTAGAATCTGAGGAGGTTCTCAGTAGATAAG 120
DB      147  TCCCATACATCGGCACAAATTTAGTGAATGAATCTGAGCGGATTCTCAGTAGACAAAG 206
QY      121  CAACCCCTACCGATTTTTCGCCCTTCCACTTTATCTCTCCCATTTATCATTCGAGCCCTTA 180
DB      207  CAACCCCTACCGATTTCTCGCTTCCATTTATCTCTCCATTTATCATATAGCAATTG 266
QY      181  CCATAGTACACCTACTGTTTCTCCAGAAACAGGATCCAAACCCCAAGGAAATCTCAT 240
DB      267  CCATAGTCCACCTACTATTCTCCAGAAACAGGCTCCAAACCCCAAGGAAATTTCTCT 326
QY      241  CAGAGGAGACAAATTCATTCACCCCTACTACTACTATCAAGATATCTTAGGAGCTC 300
DB      327  CAGACGTAGACAAATCCATTCACCCCTACTACTATCAAGATATCTTAGGAGCTC 386
QY      301  TACTATTAAATTTAAACCTCATGCTTCTAGTCCTATTCTACCGGAGCTGCTCGAGACC 360
DB      387  TCTTACTAAATCTAGCTCTAATACTACTAGTACTATTTCGACCCGAGCTCTCTCGAGACC 446
QY      361  CAGACAACTATACACCGAAACCCACTTATATACACCCCAATATCAAGCCCGAATGAT 420
DB      447  CAGATACTACACCCGACCAATCCACTCAACACACACCCCTCAGATCAAAACCCGAGTAT 506

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QY      421  ACTTCCTATTTCATGACGAATCTCCGATCAATTCCTTAACAACT 466
DB      507  ACTTCTATTTCATACGAATCTTACGATCAATCCCAACAACT 552

RESULT 12
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LOCUS      735 bp mRNA linear EST 02-JUL-2004
DEFINITION  CR451416 Day 14 bovine embryos (bcail) Bos taurus cDNA clone
bcail0012a.h.09 5', mRNA sequence.
ACCESSION  CR451416
VERSION     CR451416
KEYWORDS   EST.
SOURCE      Bos taurus (cow)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE   1 (bases 1 to 735)
AUTHORS     Renard, J.P., Sreenan, J.P. and Hue, I.
TITLE       Embryonic ESTs (bcail)
JOURNAL     Unpublished (2004)
COMMENT     Contact: Renard JP
Biologie du Développement et Reproduction
INRA
Domaine de Vilvert 78350 Jouy en Josas, FRANCE
Email: renard@jouy.inra.fr
Funding for EST sequencing was provided by an INRA funding
(AIPPP00183). Funding for the cDNA library construction was provided
by an EEC contract (BO14-CT95-0190).
The library was constructed by I. Hue, BDR, INRA, 78350
JOUY-EN-JOSAS. The double stranded cDNA was un-directionally cloned
in a TA cloning vector. bcail is a SMART cDNA library. Insert size
was between 450 and 3500 bp. Sequencing was done from the 5' end of
the clone.
Sequence cleaned of vector, adaptor and repetitions. Contact us
at signenasupport@jouy.inra.fr to obtain the chromatogram of this
sequence.

FEATURES             Location/Qualifiers
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                     /notes="Vector: pCR2.1 (Invitrogen); Clone distribution :
AGENAE Resource centre. Francois PIUMI,
Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (LREG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.73"

ORIGIN
Query Match      75.3%; Score 355.6; DB 7; Length 735;
Best Local Similarity 85.3%; Pred. No. 1.7e-93;
Matches 397; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

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QY      67  ACATCGGTACAAACCTTAGTAGAATGAATCTGAGAGGGTTCTCAGTAGATAAGCAACCC 126
DB      61  ACATCGGCACAAATTTAGTCGAATGAATCTGAGCGGATTCTCAGTAGACAAAGCAACCC 120
QY      127  TTACCCGATTTTCGCCCTTCCACTTTATCTCTCCATTTATCTCCAGCCCTTACCATAG 186
DB      121  TTACCCGATTTTCGGCTTCCATTTTATCTCTCCATTTATCATCATGACCAATGCCATAG 180
QY      187  TAGACCTACTGTTTCTCCAGAAACAGGATCCCAACACCCCAAGGAATCTCATCAGACG 246

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181 TCCACCTACTATTTCTCCAGCAAGAGGCTCCACCAACCCACAGGAATTTCTTCAGAGC 240
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307 TAATTTTAACTCCTATGCTTCTAGTCTTATCTCACCAGGCTCTTGGAGACCCAGACA 366
301 TAATTTCTAGCTCTAATTAAGTCTAGTCTTATTCGACCCGACCTCTCTGGAGACCCAGATA 360
367 ACTATACACCCAGCAACCCCTATTAACACCCCCACATATCAAGCCCGAATGATATCTCC 426
361 ACTACACCCAGCAACCCCTATTAACACCCCCACATATCAAGCCCGAATGATATCTCT 420
427 TATTTGATACCAATCTCTCCGATCAATTCCTTAACAACTAGGAGG 472
421 TATTTGATACCAATCTCTTACGATCAATTCCTTAACAACTAGGAGG 466

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RESULT 13
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DEFINITION CN789904 648 bp mRNA linear EST 26-MAY-2004
sequence.
ACCESSION CN789904.1 GI:47685884
VERSION CN789904.1
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos
1 (bases 1 to 648)
Baumann, R.G.; Baldwin, R.L., Sonstegard, T.S., Van Tassel, C.P. and
Matukumalli, L.K.
Construction and Analysis of a cDNA Library Generated From
Intestinal Muscle and Epithelial Tissues of Holstein Cattle
Unpublished (2004)
Contact: Richard G. Baumann
Bovine Functional Genomics Lab
ANRI
BLDG 162: BARC-EAST, Beltsville, MD 20705, USA
Tel: 3015048604
Fax: 3015048744
Email: rbaumann@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim_alt '' -trim fastaVector identified by
cross_match using options -minmatch 12 -minscore 12
Plate: 35 row: C column: 22
Seq primer: CCTATTAGTGACACTATAGAAC
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library in pCMVSPORT6.1, constructed from equimolar mRNA
pools derived from 5 sources, 4 lactating intestinal, 1
neonatal intestinal 4/5 lactating, Proximal Duodenum,
Jejunum, Distal Ileum, Colon, 1/5 Neonatal, Proximal
Duodenum, Jejunum, Distal Ileum"

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Best Local Similarity 85.0%; Pred. No. 2.5e-93;
Matches 397; Conservative 0; Mismatches 70; Indels 0; Gaps 0;

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QY 121 CAAACCTTTACCGGATTTTTCGCTTCCACTTTATCTCCTCCATTTATCTTGAGCCCTTA 180
Db 302 CAAACCTTTACCGGATTTTTCGCTTCCACTTTATCTCCTCCATTTATCTCAGTAGAATG 361
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Db 362 CCATAGTCCACCTACTGTTTCTCCAGGAAACAGGCTCCAAACACCCACAGGAATTTCT 421
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Db 422 CAGACGACAGCAAAATTCATTCACCCCTACTACACTATCAAGATATCTTAGAGGCTC 481
QY 301 TACTATTATTTTAAACCTCATGCTTCTAGTCTTATCTCACCAGGACCTGCTTGGAGACC 360
Db 482 TCTTACTAATTTCTAGCTCTAATTAAGTCTAGTCTTATCTCACCAGGACCTGCTTGGAGACC 541
QY 361 CAGACAACTATACACGACCAACCCACTTATATACACCCCCACATATCAAGCCCGAATGAT 420
Db 542 CAGATAACTACACCCAGCAATCCACTCAACACACACCCCTCAGATCAACCCGAGTATGAT 601
QY 421 ACTTCCTATTTCATACGCAATCTCCGATCAATTCCTTAACAACTA 467
Db 602 ACTTCCTATTTCATACGCAATCTTACGATCAATTCCTTAACAACTA 648

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sequence.
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VERSION BM435329.1 GI:18457051
KEYWORDS EST.
SOURCE Bos taurus (cow)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos
1 (bases 1 to 560)
Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Senses, C.W.,
Gordon, P.M.K. and Moore, S.S.
Gene Expression Profiling of the Bovine Gastrointestinal Tract
Unpublished (2002)
Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
Tel: 780 492 0169
Fax: 780 492 4265
Email: stephen.moore@ualberta.ca
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KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos
1 (bases 1 to 560)
Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Senses, C.W.,
Gordon, P.M.K. and Moore, S.S.
Gene Expression Profiling of the Bovine Gastrointestinal Tract
Unpublished (2002)
Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
Tel: 780 492 0169
Fax: 780 492 4265
Email: stephen.moore@ualberta.ca
Insert Length: 560 Std Error: 0.00
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Location/Qualifiers
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